STIC-Biotech/Ch mLib

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From:

Rao, Manjunath N.

Sent:

Thursday, August 22, 2002 4:49 PM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search request for 09/870113

From: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10C 01

Phone: 306-5681

Date: 8-22-02

Please search the following as soon as possible for application with serial number 09/870,113

SEQ ID NO: 1 against all commercial nucleic acid databases including issued patents database and pending application database and provide a print of all results.

SEQ ID NO: 2, 4, 8, 10, 12 against all commercial protein databases including issued patents database and pending application database and provide a print of all results.

If y u have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao, Ph.D. Biot chnology Patent Examiner Art Unit 1652, Room 10A11 Crystal Mall 1, USPTO.

Searcher: _	0.500	nveiber	
Phone:	308-	4292	
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Date Picked	Up:	8/26	
Date Compl	eted:	8/29	
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TYPE OF SEARCH:	
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Structures:	
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Patent Family:	
Other:	

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Questel/Orbit:
DRLink:
Lexis/Nexis:
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Other (specify):

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model	a: August 27, 2002, 03:57:53 ; Search time 130.92 Seconds (without alignments) 480.982 Million cell updates/sec	: US-09-870-113-2 ct score: 1940 nce: 1 MELEGRGAGGPAAGPGVYEFFKYLITKRQEEWRAGK 364	ng table: BLOSUM62 Gapop 10.0 , Gapext 0.5	ned: 562222 seqs, 172994929 residues	Total number of hits satisfying chosen parameters: 562222
OM protein	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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		Description	Q96a46 homo sapien	Q920g8 mus musculu	Q9nyz2 homo sapien	Q969q8 homo sapien	Q9h2j3 homo sapien	Q23125 caenorhabdi	Q9vay3 drosophila	Q94638 onchocerca	Q9p0j2 homo sapien	Q9cqq7 mus musculu	Q9nhy6 drosophila	Q94634 onchocerca	014281 schizosacch	Q91mj6 arabidopsis	082049 ribes nigru	064731 arabidopsis
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Query Match
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Matches 364; Conservative

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EMBL; AF288621; AAL23895-11; -
SEQUENCE 338 AA; 37510 MW; BB35B1F70C56A3FE CRC64;
                                                                                                 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA
                                         TLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQA
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Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MITOCHONDRIAL SOLUTE CARRIER-LIKE PROTEIN.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MITOCHONDRIAL RNA SPLICING PROTEIN 3/4 (PUTATIVE MITOCHONDRIAL SOLUTE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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blankaryota: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Song H., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
Song H., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
"A novel gene expressed in human hypothalamus.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF223466; AAF64141.1;
Interpro; IPR001993; Mitcoch_carrier.
Interpro; IPR001993; Mitcoch_carrier.
Fram; PP00153; mitcocarr: 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_Z.
SEQUENCE 347 AA; 37828 MW; 700DE61B230E001E CRC64;
                                                                      Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel.
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      MEDLINE-21195335; PubMed=11297739;
Li F., Nikali K., Gregan J., Leibiger I., Leibiger B., Schweyen R.,
Larsson C., Suomalainen A.;
Larston C., Suomalainen A.;
Characterization of a novel human putative mitochondrial transporter
homologous to the yeast mitochondrial RNA splicing proteins 3 and 4.";
FEBS Lett. 494:79-84(2001).
FEBML: AJ303078; CAC27997.1;
FEMBL: AF327403; AAK49520.1;
SEQUENCE 177 AA; 20045 MW; E5370283AAF732E3 CRC64;
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Primates; Catarrhini; Hominidae; Homo.
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR267854; AAG44723.1; -.
InterPro; IRR01993; Mitcoh_carrier.
Pfam: PF00153; mitco-carr; 2.
SEQUENCE 176 AA; 19931 MW; 4A4831AC572309D4 CRC64;
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Mammalia; Eutheria;
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 --NSAGHSNTLAYGASGVVATLIHDAIMNPAEVVKQRMQMAFSPYGSSLECARCVYNREG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 SLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 GGGEAGACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46
                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGGE------DEYESLPT-HSVPVHLTAGALAGAVEHCVMFPFDSVKTRMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 AGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLDVCKTLLNTQESLALNS-----HITGHITGMASAFRTVYQVGGVTAYFRGVQARVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIHPGGNSH-IANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.2%; Score 799; DB 5; Length 312; 49.5%; Pred. No. Se-61; tive 54; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Swinburne J., Ainscough R.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                     of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SROHENCE 312 AA; 34093 MW; D65FC4DD2936F76A CRC64;
Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z66521; CAA91399.1; -.
InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 FQVPATALSWSVYELFKFMLS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 YQIPSTAIAWSVYEFFKYLIT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 13, (TrEMBLrel. 13, I (TrEMBLrel. 19, I
  01,
01,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.5%
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                01-DEC-2001 (TrEMBLrel. W02B12.9 PROTEIN.
                                                                                                                     Caenorhabditis elegans.
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62 ITREGLLRPIRGASAVVLGAGPAHSLYFAAYEMTKELTAKFTSVRNLNYVISGA---VAT 118
                                                                                                                          Catmull J., Miller D.J.; "cDNAs from Onchocerca sp. encoding members of the MRS3/MRS4 class of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 TTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTL 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 INTQES-----LALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 HFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHI 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 CRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 ARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 TSCPTAMHSLMSMVKREGLLRSLKGVNAVVLGTIPAHAFYYTVYENSKAYLLN--NPRVS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Onchocerca volvulus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
                                                                           LLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 CRWPV------HLLAGSVAGLAEHCLMFPFDSVKTRLQSLCPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 SHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 ITQLTLNVPYQCTHFMIYEYMQNLLNPHHDYNPSSHLVSGGIAGGIAAAITTPLDCVKTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitochondrial solute carriers.";
Biochim. Biophys. Acta 1282:179-181(1996),
Biochim. Brophys. Acta 1282:179-181(1996),
InterPro; IPR001993; Mitoch_carrier.
Pfam: PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 303 AA; 33861 MW; 224BFA547E5D617C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MITOCHONDRIAL SOLUTE CARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
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45.2%; Pred. No. 3.7e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96326580; PubMed-8703971;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6282;
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ID Q9
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    RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashbunner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashbunner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Raradon R.C., Rogers Y.-H.C., Blazej R.G., Channew M., Pfeilfer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis N.C., Botchan M.R., Boulk J., Botsstein P., Eoritier P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Burtis N.C., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Bockon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A Glodek A., Gong F. Gorrell J.H., Wei M. F., Ibeyama C.,
RA Hostin D., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Laryer D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Havey D., Helman T.J., Wein M.-H., Ibeyam C.,
Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Luk Y., Matteri B., Morfntch T.C., McLeod M.P., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Randson D.R., Marten B., Martis H., Weissen D.,
RA Balazolo M., Pittman G.S., Pan S., Pollard J., Weissen D.,
Rayersas R., Mender E., Wassarman D.A., Mellams S., Yang S., Yang S., Yao O.A.,
Spler E., Spradling A.C., Stapleton M., Strong R., Santh T.,
Railams R., Wayes M., Woodage T., Worley K., Wu D., Yang S., Yao O.A.,
Railams R., Wassarman D.A., Walanstock G.M., Weissenbach J.,
Railams R., Wassarman D.A., Weiller E., Wassarman D.A., Walanstock G.M., Weilsenbach S.,
Railams R., Wassarman 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 DYESLPT-TSVGVNWTAGAIAGVLEHVVWYPLDSVKTRMQSL--SPPTKNMNIVSTLRTM 61
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SEQUENCE FROM N.A.
STRAIN-Y, CN BW SP.
STRAIN-Y, CN BW SP.
STRAIN-Y, CN BW SP.
Champe M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungail C.J.,
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
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EMBL; AE003763; AAF56764.1; -.
EMBL; AY060268; AAL25307.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.3%; Score 781; DB 5; Length 379; 52.7%; Pred. No. 2.3e-59; ive 41; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00215; MITOCH_CARRIER; 2.
Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 379 AA; 41794 MW; F6A20BABA35F5C2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0039561; CG4963.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
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Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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Pfam; PF00153; mito_carrier.
PRINTS; PR00253; mito_carr; 3.
PRINTS; PR00205; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 380 AA; 41844 MW; ACGARATORDATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
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                                                                                                                                                                                                                                                                                                                                          Matches 131; Conservative
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MEDLINE-2108560; PubMed=11217851;
MEDLINE-2108560; PubMed=11217851;
MEDLINE-2108560; PubMed=11217851;
Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Euruno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                179 VATLIHDAAMNPAEVVKORMOMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 QAIHFWTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 -SHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQ 357
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                       Euteleostomi;
                                                                                                                                                                              W., Xu
                                                                                                                                                                                                                                                                                                                                                                     37.4%; Score 725.5; DB 4; Length 187; 71.9%; Pred. No. 5.7e-55; tive 27; Mismatches 24; Indels 1
                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordáta; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                        Huang Q., Yu.Y., Huang C., Jiang C., Ren S., Zhou J., Gu Wang Y., Fu G., Chen Z., Han Z.;

"A novel gene expressed in human adrenal gland.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF155660; AAF07479.1;

InterPro; IPR001993; Mitoch_carrier.

InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                    24; Indels
                                                                                                                                                                                                                                                                                                           PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
SEQUENCE 187 AA; 21125 MW; 26F760526F7DE21B CRC64;
            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MITOCHONDRIAL SOLUTE CARRIER.
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                              Pfam; PF00153; mito_carr; 2. PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 71.9
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                TISSUE=ADRENAL GLAND;
                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                  NCBI_TaxID=9606;
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Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Rawaji H., Rohtsuki S.,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPF 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 -SHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQ
                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK015770; BAB29969.1; -
EMBL; AK015770; BAB24436.1; -
MGD; MGI:1914962; 1700020E22Rik.
InterPro; IPR001993; Mitoch_carrier.
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Schmid K.J., Tautz D.;
"A screen for rapidly evolving genes from Drosophila.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF211402; AAR73387.1; -.
FlyBase; FBGn0039561; CG4963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfan: PF00153; mito_carr; 2.
PRINTS; PR00926; MITOCARRIER.
PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN 1.
SPONTE: PS00215; MITOCH_CARRIER; UNKNOWN 1.
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380 AA; 41844 MW; 4C9AA524B97F8C6C CRC64;
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 41.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.2%; Score 722.5; DB 11;
71.2%; Pred. No. 1e-54;
tive 30; Mismatches 22;
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Conservative
                                                                                             PRELIMINARY;
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                                                                                                                                                                                                  Schizosaccharomyces.
NCBI_TaxID=4896;
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164
208
303 AA;
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Best Local Similarity
Matches 116; Conserv
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TRANSMEM 1:
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TRANSMEM
SEQUENCE
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Q9LMJ6;
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Q9LMJ6
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                                                                                                                                                                   IHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSH 300
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                                                                                 IRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMOSLQPDPA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 ARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSY 228
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                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                  of the MRS3/MRS4 class
                                                     Onchocerca gibsoni.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                49;
                                                                                                                                                                                                                       301 ITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLI 353
Length 380;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        mitochondrial solute carriers.";
Biochim. Biophys. Acta 1282:179-181(1996).
EMBL; U45997; AAB19036.1; -.
Interpro; IPRO1993; Mitoch_carrier.
Pram; PF00153; Mitoc, Carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 301 AA; 34176 MW; COBA8D819FB8EA79 CRC64;
                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.7%; Score 672.5; DB 5;
43.2%; Pred. No. 4.1e-50;
ative 51; Mismatches 83;
 DB 5;
         2e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                      Catmull J., Miller D.J.; "CDNAs from Onchocerca sp. encoding members
                                                                                                                                                                                                                                                                                  301 AA
                    41; Mismatches
37.0%; Score 717.5; 49.5%; Pred. No. 7.2
                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=96326580; PubMed=8703971;
                                                                                                                                                                                                                                                                                                                                     MITOCHONDRIAL SOLUTE CARRIER.
                                                                                                                                                                                                                                                                                                                                                                    Onchocercidae; Onchocerca,
NCBI_TaxID=6284;
                    Conservative
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Best Local Similarity
Matches 139; Conserv
          Similarity
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          Local Simples 145;
 Query Match
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                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 DYEALPAGATVTTHWVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-972;
Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 LLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAI
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 303;
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69975CDE18107AB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                SPAC8C9.12C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetaceae; Schizosaccharomycetales; Schizosaccharomycetaeee;
228 LNTQQTPASIPHIDCSHKASLQHITKGWLTELNHLLPSRYRWI----
                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE MITOCHONDRIAL CARRIER C8C9.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.0%; Score 601; DB 3; 39.5%; Pred. No. 6.3e-44; iive 63; Mismatches 109;
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PROSITE; PS00215; MITOCH_CARRIER; 3.
Hypothetical protein; Mitochondrion; Inner
                                                                                                                                                                                                                                          303
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POTENTIAL.
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                                                      333 IYQIPSTAIAWSVYEFFKYLIT
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Job time: 1287 sec
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A Sakano H., Toriumi M., Chung M., Goldsmith A., Liu A., Liu A.,
A Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,
A Conway A., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B.,
A Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
B Ecker J.R., Federspiel N.A., Theologis A.;
The sequence of BAC Floki from Arabidopsis thaliana chromosome 1.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
B EMBL, ACGORDSJ, ARE 2217.1;
InterPro; IPR001993; Mitcoh_carrier.
R InterPro; IPR001993; Mitcoh_carrier.
R PRINTS; PR00266; MITCOHRIER.
R PRINTS; PR00215; MITCCH_CARRIER; UNKNOWN_2.
C SEQUENCE 781 AA; 87081 MW; 9FB579B9BD746D1E CRC64;
                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 PDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 AFYRSYTTQLTMNVPFQAIHFWTYEFLQE---HFNPQRRYNPSS---HVLSGACAGAVAA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 AFYASYRTTVLMNAPFTAVHFATYEAAKKGLMEFSPDRISDEEGWLVHATAGAAAGGLAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 AATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 AVTTPLDVVKTQLQCQGVCGCDRFTSSSI---SHVLRTIVKKDGYRGLLRGWLPRMLFHA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 PVRQDPD-----SGPDY--EALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Saxifragales; Grossulariaceae; Ribes.
NCBL_TaxID=78511;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGG -- NSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 781;
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                 Last sequence update)
Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MITOCHONDRIAL CARRIER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                          26.9%; Score 521; DB 10;
39.4%; Pred. No. 1.8e-36;
live 44; Mismatches 123;
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   Created)
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01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 39.48
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: || || || || PAAAICWSTYEGVLY 314
                                                                                                                                                                  SEQUENCE FROM N.A.
                                             F10K1.26 PROTEIN. F10K1.26.
                                                                                                                                    NCBI_TaxID=3702;
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082049
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60 AMGLGAGPAHAVYESVYEMCKETES---HGDPSNSGAHAVSGVFATVASDAVITPMDVVK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 VTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 FNPQ--RRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 VSPETANDENLLVHATAGAAAGALAAVVTTPLDVVKTQLQCQGVCGCDRFSSSSIQDVIG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:||::|| :|| || |||:| :||:|:|:
| MIAGSIAGSIEHMAMYPVDTLKTRIQAI-GSCSAQSAGLRQALGSILKVEGPAGLYRGIG 59
                                                                                 QRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQE---H
                                                                                                                                                                                                                                                                                                                                                                                                                    26.3%; Score 510; DB 10; Length 289; 39.6%; Pred. No. 4.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQE 358
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                                                                                                                                                                                                                                                                                                   47; Mismatches 115;
                                                      W.
                                                      hesis (1995), University of Dundee,
SEQUENCE FROM N.A.
STRAIN-CV. BEN ALDER; TISSUE=FRUIT;
Woodhead M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 114; Conserv
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Search completed: August 27, 2002, 04:19:20

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Human protein SEQ Human polypeptide, Human mitochondria Human protein SEQ Drosophila melanog

mitochondria

Human Human

polypeptide,

Human secreted pro O. volvulus mitoch

Human secreted proGene #25 human sec
Blackcurrant RIB7
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Arabidopsis malana
Human ORFX ORF2730
Human ORFX ORF2732
Human ORFX ORF2728
Novel human diagno
Drosophila melanog
Drosophila melanog
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Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Drosophila melanog

polypeptide polypeptide ORFX ORF2547

Human uncoupling

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Searched:

Database

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Result Š.

Seguence:

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
AAM79039
ABB61130
AAM80023
AAM93909
AAB98222
                                                                            AAB49665
AAB32112
AAB321112
AAB32111
AAU10988
AAG22077
AAG422078
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AAG22079
AAG43094
AAB42966
AAB42968
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ABG01167
ABB69108
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AAM40959
AAM40960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 6436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
 WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM41505
 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human uncoupling p
Human transport pr
Human polypeptide
Human bone marrow
Human ORFX ORF2744
Human new mitochondria
Novel human secret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted pro
ORFX ORF398
mitochondria
                                                                                                                          (without alignments)
291.835 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21051/900data/geneseq/geneseqp-embl/AA1980.DAT:*
21051/900data/geneseq/geneseqp-embl/AA1981.DAT:*
21151/900data/geneseq/geneseqp-embl/AA1991.DAT:*
21151/900data/geneseq/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                   1 MELEGRGAGGVAGGPAAGPG......VYEFFKYLITKRQEEWRAGK 364
                                                                                                         August 27, 2002, 02:34:08; Search time 138.54 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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Human
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                 747574 segs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
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AAB50383
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AAM39719
AAM00938
AAB42980
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AAU29748
AAU01989
AAB40634
AAB98221
                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_032802:*
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Maximum DB seq length: 2000000000
                                                                                                                                                                    US-09-870-113-2
1940
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289
289
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366
372
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Match 1
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1534
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Matches
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  NEW MARKET MARKE
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                                                                                                                                                                                                                                                                                                                           the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                               system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, auch as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotextic/chemokinctic activity, nemoratic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed
                                           Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYFIDCVKTRMQSLQPD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYR 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVY 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                         to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 gacrppvrqdpdsgpdyealpagatvtthmvagavagilehcvmypidcvktrmqslqpd 60
                                             Wang
                                                                                                                                                                                              useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCK
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Zhang J;
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                                        Oian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.4%; Score 1696; DB 22;
100.0%; Pred. No. 1.6e-163;
iive 0; Mismatches 0;
                                        Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 6436; 10078pp; English.
                                                                                                                                                                                            polypeptides, us
system injuries
                                        Asundi V, Che
Wehrman T, Xu
, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB50383 standard; Protein; 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human uncoupling protein #6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFFKYLITKRQEEWRAGK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.C
Matches 318; Conservative
                                                                                                                                                                                            Novel nucleic acids and such as central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates
                                                                                                                            2001-442253/47.
                                        Liu C, A
Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 AA;
(HYSE-) HYSEQ INC.
                                                                                                                                                   N-PSDB; AAI60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification.
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                                      YT,
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                                           Tang
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                                                                                      Zhao
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antirheumatic; antiproliferative; cardiant; vasotropic; cerebroprotective; neuroprotective, antibacterial; opthalmological; gastrointestinal; nephrotropic; gynaecological; vulnerary; thrombolytic; gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a human uncoupling protein. The nucleotide sequences encoding the uncoupling proteins may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 VTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uncoupling proteins and nucleic acid sequences encoding them, useful for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 QRMOMYNSPYHRVTDCVRAVWONEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 QRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 289;
uncoupling protein; immunosuppressive; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 YQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQEEWRAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.1%; Score 1534; DB 21; 100.0%; Pred. No. 3.8e-147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ni J, Komatsoulis G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 323-324; 343pp;
                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0142821.
99US-0149448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                              99US-0128701.
                                                                                                                                                                                                                                                                                                                                       2000WO-US09534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0164751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC90457
                                                                                                                                                                                                                                     WO200061614-A2
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                          06-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                              09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-1999;
18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1999;
                                                                                                                                infertility
                                                                                                                                                                                                                                                                                         19-OCT-2000
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AAM39719 standard; Protein; 268 AA.
                                                                                 Human polypeptide SEQ ID NO 2864.
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0663191.
2000US-0693036.
2000US-0693036.
                                                                                                                                                                                                                                       26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                           2000US-0488725
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                              Zhou P,
                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAI58875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assays for recept. C.N.S disorders.
                                                                                                                                                                                                WO200153312-A1
                                                                                                                                                                                                                                                                    25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                 03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification
                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                           21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                 29-NOV-2000;
                                                              22-OCT-2001
                                                                                                                                                                                                                   26-JUL-2001
                                                                                                                                                        leukaemia.
                                         AAM39719;
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                                                                                                                                                                                                                                                                                                                                                                                              Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
  RESULT
AAM39719
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences for 43 novel human transport proteins (designated TPPTs). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative
                                                                                Human; transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder; immune disorder; cancer.
                                                                                                                                                                                                                                                                               ż
                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide with a human transport protein sequence is useful for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 QRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 VTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 QRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 mvagavagilehcvmypidcvktrmqslqpdpaaryrnvlealwriirteglwrpmrgln 60
                                                                                                                                                                                                                                                                               Burford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 289;
                                                                                                                                                                                                                                                                              JL, Tang YT, Bandman O, Au-Young J, Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 YQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQEEWRAGK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1534; DB 22;
Pred. No. 3.8e-147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.1%; Score __ 3.8/
100.0%; Pred. No. 3.8/
**** 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 133-134; 165pp; English.
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                                                                                                                                                                                                                                                                             Hillman
AAB60113 standard; Protein; 289
                                                                                                                                                                                                                                                                                       Lu DAM,
                                                             Human transport protein TPPT-33
                                                                                                                                                                                                       99US-0139923.
99US-0148177.
99US-0149357.
99US-0162287.
                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                    16-JUN-2000; 2000WO-US16668
                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders such as cancer
                                                                                                                                                                                                                                                                              Ή,
                                                                                                                                                                                                                                                                                       Azimzai Y,
                                                                                                                                                                                                                                                                              Xue
                                                                                                                                                                                                                                                                                                           WPI; 2001-041424/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AA;
                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF27733
                                                                                                                                           WO200078953-A2
                                                                                                                                                                                                                                                                              Yang
                                                                                                                         Homo sapiens
                                                                                                                                                                                                       17-JUN-1999;
10-AUG-1999;
                                        28-MAR-2001
                                                                                                                                                                                                                             .8-AUG-1999;
                                                                                                                                                                                                                                      28-OCT-1999;
                                                                                                                                                                28-DEC-2000
                                                                                                                                                                                                                                                                                       Baughn MR,
                     AAB60113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                  peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Hauntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ren F, W.
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
nootropic; immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and thrombolytic activity, cancer diagnosis and therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.5%; Score 1387; DB 22; Best Local Similarity 98.1%; Pred. No. 2.9e-132; Matches 262; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO 2864; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Asundi V, Chen R, Wang Z, Wehrman T, Xu C,
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98 TRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKK 157

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The present sequence is one of 251 novel human polypeptides encoded by a bone marrow-expressed polynucleotide. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HVV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation
                                                      218 NEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAA 277
                                                                                                             278 ATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIP 337
                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; bone marrow, antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
158 TLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Asundi V, Chen R, Ma Yu C, Xue AJ, Yang Y, Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow protein, SEQ ID NO: 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 504-505; 648pp; English.
                                                                                                                                                                                                                         338 STAIAWSVYEFFKYLITKROEEWRAGK 364
                                                                                                                                                                                                                                                                                                         AAM00938 standard; Protein; 366 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Werhman T, X
Drmanac RT;
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2000US-0552317
2000US-0598042.
2000US-0653450.
2000US-0653450.
2000US-0653191.
2000US-0653933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-2000; 2000WO-US34960
                                                                                                                                                                                                                                                                                                                                                              01-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ford JE,
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antidiabetic; antidianemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                          73 TIHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMR 132
                                                                                                                                                                                                                                                                                                                                                                               252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 FNPORRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALN-SHITGHITGMASA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEH
                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                        DB 22; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 FRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQEEWRA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 1113.5; DB 22; Lengt; Pred. No. 2.6e-104; 43; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ORFX ORF2744 polypeptide sequence SEQ ID NO:5488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB42980 standard; Protein; 272 AA.
                                                                                                                                                                                                                        57.4%;
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99US-0127636.
99US-0127728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                        Local Similarity
nes 202; Conserv
                                                                                                                                                                      366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200058473-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000;
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05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000
                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB42980;
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The invention relates to a novel human mitochondrial solute carrier protein, hMSC-o (AAB60658), and cDNA encoding it (AAF59920). hMSC-o is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-o proteins and nucleic acids, and the detection of hMSC-o proteins and nucleic acids in a sample. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 VKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human mitochondrion solute carrier protein and its nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 GVGRGAGGGEAGACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WONEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVA
                                    Human mitochondrial solute carrier protein; hMSC-o; hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 aaattpldvcktllntqenvalslanisgrlsgmanafrtvyqlnglpa 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
   Human mitochondrial solute carrier protein hMSC-o.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                     (SREN-) SOUTHERN RES CENT NAT HUMAN GENE GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.2%; Score 1012.5; Di
65.1%; Pred. No. 4e-94;
ive 39; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 20; 21pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU29748 standard; Protein; 677
                                                                                                                                                                                   17-MAR-2000; 2000CN-0114958
                                                                                                                                                                                                                    17-MAR-2000; 2000CN-0114958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents hMSC-o.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 188; Conservative
                                                   preparation; detection
                                                                                                                                                                                                                                                                                                                   WPI; 2001-050544/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 AA;
                                                                                                                                                                                                                                                                                     Gao X,
                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAF59920
                                                                                    Homo sapiens.
                                                                                                                 CN1269409-A
                                                                                                                                                  11-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                  Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU29748;
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which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
costeopathic; anticonvulsant; antiarthritic; immunosuppressant;
limunostimulant; cardiant; thrombolytic; coaquiant; vasotropic;
antidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; and intanaemic. The sequences can be used for determining
the presence of or predisposition to, or preventing or treating
the presence of or predisposition to, or preventing or treating
the presence of or predisposition to, or preventing or treating
the proteins and nucleic acids may be used to treat cancers,
proliferative disorders, neurodegenerative disorders, osteoarthritis,
cypertension, hypothyroidism, cholesterol ester storage, systemic lupus
erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
bacterial or fungal infection, malaria, autoimmune disorders, asthma,
allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
coagulation; to inhibit thrombosis; and as a contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 VKTRMQSLQPDPAARYRNVLEALWRIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAV 215
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                                                                                                                                               Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.9%; Score 1025.5; DB 69.4%; Pred. No. 1.5e-95; ive 41; Mismatches 40
                                                                                                                                                                                                               Claim 11; Page 4662-4663; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIPSTAIAWSVYEFFKYLITKRQEEWRA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB60658 standard; Protein; 331 AA
30-MAR-2000; 2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 69.4
Matches 186; Conservative
                                                                 Leach M;
                                (CURA-) CURAGEN CORP.
                                                                                                WPI; 2000-602362/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 AA;
                                                                                                                N-PSDB; AAC77189
                                                                 Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB60658;
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Gaps 95 215

275

us-09-870-113-2.rad

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. They may be used to the proteins are useful in genetic vaccination, testing and increase stem cell proliferation; to requiate haematopoissis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU2510-AAD3304 represent the amino acid in treatment of leukaemias. AAU2510-AAD3304 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S;
                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALN-S 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 919; DB 22;
Pred. No. 3.4e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 189; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.48;
                                                                                                                                                                                                                                                              Liu C, Drmanac RT;
                                                                                                                                      16-APR-2001; 2001WO-US08656
                                                                                                                                                                       18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 181; Conservative
                                                                                                                                                                                                                                                                                               WPI; 2001-611725/70.
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                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            677 AA;
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                                                                  WO200179449-A2.
                                   Homo sapiens
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                                                                                                     25-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Best Local 9
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and of the invention. Secreted proteins and their related nucleic acids can be used in the diagnosis of or susceptibility to a pathological condition by determining the presence or absence of a mutation in a nucleic acid or the presence or absence of a mutation in a condition by determining the presence or absence of a mutation in a condition by determining the presence or absence of a mutation in a condition in e.g. humans, mice, rabbits, goats, horses, cat's, dogs, chickens or sheep. The antibodies to the polypeptides can also be used in alteriating symptoms associated with disorders and in diagnostic alleviating symptoms associated with disorders and in diagnostic confittion in e.g. humanossays or enzyme linked immunosorbent assays (ELISA). The disorders include autoimmune diseases e.g. rheumatoid atthiutis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The peptides can also fungi and ocular disorders e.g. corneal infection. The peptides can also be used to aid wound healing and epithelial cell proliferation, to help prevent skin ageing due to sunburn, to maintain organs before transplantation, to regenerate tissues, in chemotaxis and as a food additive or preservative to alter storage capabilities.
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                                                                                                                                                                                                               Human secreted protein; autoimmune disorder; hyperproliferative disorder; cardiovascular disorder; angiogenesis; envious system disorder; bacterial infection; viral infection; fungal infection; ocular disorder; wound healing; tissue regeneration; epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forty one nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents a human secreted protein encoded by a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.2%; Score 916; DB 22;
100.0%; Pred. No. 1e-84;
tive 0; Mismatches 0;
                                                                                                                                                                          Human secreted protein encoded by gene #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 501; 518pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA;
                                           AAU01989 standard; Protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2000; 2000WO-US26324.
                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Komatsoulis G, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-281684/29.
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                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                               29-AUG-2001
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                                                                                    AAU01989;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antlinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                         vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthriic; immunosuppressant; cardiant, immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
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                                                                      354
                                                                                         301 ITCHITGMASAFRIVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
                                                                                                                                                                                                                                                                                                                                                                     Human ORFX ORF398 polypeptide sequence SEQ ID NO:796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 854; 5507pp; English.
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                                                                                                                                                                                                                                AAB40634 standard; Protein; 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimkets RA,
                                                                                                                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2000
                                                                                                                                                                                                                                                                            AAB40634;
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graft vs host disease, cardiovascular disease, diabetes mellitus, hypethyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                    193 VVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEH 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAF 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human mitochondrial solute carrier (hMSC) protein isomer and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a human mitochondrial solute carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein, designated hMSC-homologue, which is expressed in human hypophysis. Also described are methods for the preparation and detection of hMSC-homologue protein and nucleotide sequences. The present sequence represents hMSC-homologue, as given in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human mitochondrial solute carrier (hMSC-homologue) protein SEQ:7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQEEWRAGK 364
                                                                                                                                                                                                                                                                                           Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; hMSC; hMSC-homologue; mitochondrial solute carrier.
                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                       4.2e-84
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                                                                                                                                                                                                                                                                          46.9%; Sco. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 18 (disclosure); 22pp; Chinese.
                                                                                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB98221 standard; Protein; 176 AA.
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                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 AA;
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                                                                                                                                                                                                                                                                                                                                                Matches 172;
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                                                                                                                                                                                                                     Sequence
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WPI; 2001-656860/75
                                                                                          Similarity
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                                             299 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                             ABB61130;
                                                                              Query Match
                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ma Y;
                                  193 VVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEH 252
                                                                             253 FNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAF 312
                                                                                          Gaps
                                                       5 vvkgrmgmynspyhrvtdcvravwqnegagafyrsyttqltmnvpfgaihfmtyeflgeh 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities.
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                                                                                                                       Liu C, Drmanac RT, Asundi V, 2hou P, Xu C, Ca
Wang D, Wang J, Zhang J, Ren F, Chen R, Wang
Yang Y, Wejhrman T, Goodrich R;
              Indels
                                             0
   Pred. No. 4.2e-84;
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 4043; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in diagnosis and gene therapy
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2000US-0560875.
2000US-0598075.
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2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
100.08;
                                                                                                                                                                                                                                                                         Human protein SEQ ID NO 1701
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                                                                                                                                                                                                                                                   (first entry)
            Matches 172; Conservative
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  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAK52172
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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20-JUN-2000;
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20-OCT-2000;
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                                                                                                                                                                                                                             AAM79039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
                                                                                                                                                                                                                                                                                                                                               1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 60
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28 melr---sgsv--gsgavarrmdgds------rdggggg-----kdatgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                     Length 299;
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                                                                                                                                                                                                                  44.1%; Score 856.5; DB 22; 59.6%; Pred. No. 2.4e-78;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                       Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
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(HELI-) HELIX RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                             353 ITKRQEEWRA 362
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                                                                                                                                                                                                                                199 AA;
                      N-PSDB; AAK53156
                                                                                                                                                                                  inflammation.
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                                                                                                                                                                                                                                Sequence
                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                           182 LLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAI 241
                                                                                                                                           DYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRI 121
                                                                                                                                                                                122 IRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                         HFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHI 301
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ma
                                                                                                                                                             5 dyeslpt-tsvgvnmtagajagvlehvvmypldsvktrmgsl--spptknmnivstlrtm 61
                                                                                                                                                                                                                               Cao Y,
                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu C, Cao Y
R, Wang ZW;
                                                                                                                                                                                                                                                                                             Length 379;
                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Asundi V, Zhou P,
Wang J, Zhang J, Ren F, Chen
Wejhrman T, Goodrich R;
                                                                                                       Score 781; DB 22;
Pred. No. 1.5e-70;
                                                                                                                          41; Mismatches
                                                                                                                                                                                                                                                                                                                                                              AAM80023 standard; Protein; 199 AA
                                                                                                      40.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein SEQ ID NO 3669.
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2000US-0560875.
2000US-0598075.
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2000US-0693325.
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2000US-0654936.
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                          Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C, D
Wang D,
Yang Y, W
                                                                                                                 Local Similarity
                                                                           379 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157190-A2
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20-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2000;
01-SEP-2000;
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20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                AAM80023;
                                                                             Sequence
                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
Zhao QA,
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                                                                                                                                                                       The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78223-AAM80302) that exhibit activity elating to cytokine, cell proliferantian or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activithinhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLALN-SHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 GAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 MNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.1%; Score 739.5; DB 22; Best Local Similarity 71.6%; Pred. No. 1e-66; Matches 136; Conservative 27; Mismatches 26;
                                                                                                        Page 409-410; 6221pp; English.
Nucleic acids encoding polypeptides wuseful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM93909 standard; Protein; 187 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-2000; 2000EP-0114089.
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11-JAN-2000; 2000JP-0118774.
02-MAX-2000; 2000JP-0183765.
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The invention relates to primers for synthesising full length CDNA clones. 830 CDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5'- and 3'-ends of the CDNA molecules have been determined. For synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched CDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length CDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                              830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation \cdot
                                           Η;
                   Hayashi K, Ishii S, Kawai Y;
K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                               Claim 8; SEQ ID NO 4059; 1380pp + sequence listing; English.
                   Isogai T,
a T, Nagai
                                     Wakamatsu A, Sugiyama T,
                   Nishikawa T,
                                                                              WPI; 2001-524255/58.
N-PSDB; AAK94871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                   Ota T,
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ij 179 VATLIHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLIMNVPF 238 QAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALN 298 -SHITGHITGMASAFRIVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQ 357 1; Gaps 37.4%; Score 725.5; DB 22; Length 187; 71.9%; Pred. No. 2.4e-65; Live 27; Mismatches 24; Indels 1; 24; Indels Best Local Similarity 71.9% Matches 133; Conservative EEWRA 362 | || |enra 185 Query Match 239 61 358 ð g ò 엽 à Q ò

Search completed: August 27, 2002, 03:55:57 Job time: 4909 sec

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Sequence

Sequence 37, 18 Sequence 37, 18 Sequence 37, 18 Sequence 37, 18 Sequence 10, 18 Sequence 29, 18 Sequence 29, 19 Sequence 29, 19

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ZIP: 194.06-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                                                                                               US-09-068-140A-15
Sequence 15, Application US/09068140A
Patent No. 6281409
GENERAL INFORMATION:
APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
APPLICANT: and Rex Michael Brennan
TITLE OF INVENTION: Blackcurrant Promoters and Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
          US-08-518-878B-51
US-08-807-861A-51
US-09-210-681-51
US-09-210-681-51
US-08-946-719A-51
US-08-946-719A-51
US-08-14-878B-35
US-08-470-868A-56
US-08-807-868A-37
US-08-807-868A-37
US-08-961-871-10
                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILLING DATE: NO. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Ribes nigrum ; STRAIN: Ben Alder US-09-068-140A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
 MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                    171.5
171.5
171.5
1168.5
139.5
139.5
139.5
139.5
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139.5
139.5
101.5
101.5
August 27, 2002, 02:37:18 ; Search time 48.11 Seconds (without alignments) 184.804 Million cell updates/sec
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Sequence 2, Appl
Sequence 2, Appl
Sequence 12, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 2, Appl
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                                                                                                                                               US-09-870-113-2
1940
1 MELEGRGAGGVAGGPAAGPG......VYEFFKYLITKRQEEWRAGK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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Compugen Ltd
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US-09-068-140A-10
US-09-068-140A-10
US-09-08-140A-10
US-09-234-613-19
US-09-160-119-4
US-09-160-119-4
US-09-160-119-4
US-09-109-132
US-08-375-009-33
US-08-775-009-33
US-08-9775-009-33
US-08-9775-009-33
US-09-172-528-4
US-09-172-528-2
                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                231628 segs, 24425594 residues
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              GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                  using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
                                                                  protein search,
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Perfect score:
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MOLECULE TYPE:
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                                                                                                          61 PDYEALPA--GATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEAL 118
                                                                                                                                                                                   119 WRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC 178
                                                                                                                                                                                                                                                               179 VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPF 238
                                                                                                                                                                                                                                                                                                                                          239 QAIHFMTYEFLQE---HFNPQ--RRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQE 293
                                                                                                                                                                                                                                                                                                                                                                                                                 294 SLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLI 353
                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09068140A

Sequence 10, Application US/09068140A

Patent No. 6281409

GENERAL INFORMATION:

APPLICANT: MATY Rose Woodhead, Mark Andrew Taylor

APPLICANT: and Rex Michael Brennan

TITLE OF INVENTION: Blackcurrant Promoters and Genes

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Smithfaline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STRATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER: Thoppy disk

COMPUTER: DeathIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION NUMBER: US/09/068,140A

FILING DATE:

CLASSIFTRATTON:
                                 26.3%; Score 511; DB 4; Length 328; 38.4%; Pred. No. 3.1e-44; Live 48; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: No. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
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3ER: C70237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C7/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 289 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                     Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 AMGLGAGPAHAVYFSVYEMCKETFS---HGDPSNSGAHAVSGVFATVASDAVITPMDVVK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 QRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQE---H 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 FNPQ--RRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 VTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVK 195
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                  ; Score 510; DB 4; Length 289;
; Pred. No. 3.2e-44;
47; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 AFRIVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQE 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 ---SIVKKNGYVGLMRGWIPRMLFHAPAAAICWSTYEASKTFFQKLNE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCORNATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: An-Young, Janice
APPLICANT: We, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Grelpr, Karl J.
APPLICANT: Grelpr, Rarl J.
APPLICANT: HUMAN REGULATORY WOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS SOFTWARE: Fast-SEO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/933,750C FILLING DATE: September 23, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/08933750C Patent No. 5932442
                                                                                                                                                                                                                                                  Query Match 26.3%;
Best Local Similarity 39.6%;
Matches 114; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                             N-terminal
                                                                                                                           ; ORGANISM: Ribes nigrum
; STRAIN: Ben Alder
US-09-068-140A-10
peptide
YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: Septemb
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                         HYPOTHETICAL: YES ANTI-SENSE: NO FRAGMENT TYPE: NOORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
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APPLICATION NUMBER: US/09/234,613
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Sequence 4, Application US/09160119A

Patent No. 6316219

GENERAL INFORMATION:

APPLICANT: STEPHANE

APPLICANT: SOUCHET, MICHEL

APPLICANT: BRIL, ANYOINE

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GH-30985
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 351 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MARDIATE SOURCE:
LIBRARY: SYNOOAT01
CLONE: 724157
US-09-234-613-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 CLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHEGTRTLW --- SGLPAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 ATGAGPAHALYFACYEKLKKTL----SDVIHPGGNSHIANGAAGCVATLLHDAAMNPA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 EVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQE 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 ITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQEE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INCRMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corley, Nail C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.1%; Score 293; DB 2; I ilarity 25.1%; Pred. No. 7.7e-22; Conservative 50; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Incyte Pharmaceuticals, Inc
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Patent No. 6132973
                                                                                                                              INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Incyte Pharmacet.
Incyte Pharm
TELECOMMUNICATION INFORMATION:
                                                         TELEFAX: 415-845-4166
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US-08-933-750C-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 89; Conserv
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US-09-234-613-19
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110 ------LWRPMRGLNVT 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 LVMTVPATAIYFTAYDQLKAFLCGRALTSDLYAP------MVAGALARLGTVTVISPL 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 HFN----PQRRYNPSSHVLSGACAGAVAAATTPLDVCKT----LLNTQESLALNSHITGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 VDSTWLLLRRIRAESGTKGLFAGFLPRIIKAAPSCAIMISTYEFGKSFFGRLNQD 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.1%; Score 293; DB 4; L
Best Local Similarity 25.1%; Pred. No. 7.7e-22;
Matches 89; Conservative 50; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 PAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA-
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EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
SARLIER FILING DATE: 1998-07-02
SOFTWARE: FSC ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                    PF-0356 US
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                               US/08/933,750
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241 IHFMTYEFLQEHF-NPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNS 299
                                                  63 YEALPAGATVTTHM--VAGAVAGILEHCVMYPIDCVKTRMQSLQ------PDPAARYRNV 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
                                                                                                                                             300 HITCHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFK 350
                                                                                                                                                                                     : :|: || : : | | : : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SISTEM: DOS
SOFTWARE: FRASLEGO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0356 US
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Patent No. 5932442
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ATTORNEY/AGENT:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lal, Preeti
Hillman, Jennifer
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 24.77
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LIBRARY: SPLNNOT02; CLONE: 207452
US-08-933-750C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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APPLICANT: Lal, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94304
                                                                                                                                                                                                                                                                                                                                                        US-08-933-750C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     135 NVTATGAGPAHALYFACYEKLKKTLSDVI-----HPGGN-----SHIANGAAGCVATLLH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 LPQLLGVAPEKA-----IKLTVNDFVRDKFMHKDGSVPLAAEILAGGCAGGSQVIF- 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 DAAMNPAEVVKQRMQMYNSPYHRVTDCVR----AVWQNEGAGAFYRSYTTQLTMNVPFQA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAVAGILEHCVMYPIDCVKTRMQSLQPDPA----ARYRNVLEALWRIIRTEGLWRPMRGL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 GSVAGAVGATAVYPIDLVKTRMQNQRSTGSFVGELMYKNSFDCFKKVLRYEGFFGLYRGL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 NVTATGAGPAHALYFACYEKIKKTLSDVI-----HPGGN-----SHIANGAAGCVATLLH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPQLLGVAPEKA-----IKLTVNDFVRDKFWHKDGSVPLAAEILAGGCAGGSQVIF- 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAAMNPAEVVKQRMQMYNSPYHRVTDCVR----AVWQNEGAGAFYRSYTTQLTMNVPFQA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TNPLEIVKIRLQVAG----EITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFSA 497
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 IHFMTYEFLQEHF-NPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : :|: || : : | | :: | 331 Y-----SGVIDCFRKILREEGPKALWKGAGARVFRSSPQFGVTLLTYELLQ 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 HITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFK 350
                                                                                                                                                                                                                                               Length 447;
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                                                                                                                                                                                                                                               ; Score 265; DB 4; Length 44; Pred. No. 8.3e-19; 47; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CENERAL INFOGRATION

APPLICANT: SOUCHET, MICHEL
APPLICANT: SOUCHET, MICHEL
APPLICANT: SOUCHET, MICHEL
APPLICANT: BILL, ANTOINE
FILE REFERENCE: GH-30985
CURRENT APPLICATION UNMER: US/09/160,119A
CURRENT APPLICATION UNMER: US/09/160,119A
CURRENT APPLICATION UNMER: EP 97402511.6
EARLIER APPLICATION NUMBER: EP 94401655.0
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09160119A Patent No. 6316219 GENERAL INFORMATION:
                                                                                                                                                                                                                                                   13.7%;
28.2%;
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Best Local Similarity 28.2%
Matches 82; Conservative
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 28.29
Matches 82; Conservative
                                                                    TYPE: PRT
CORGANISM: HOMO SAPIENS
US-09-160-119-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: HOMO SAPIENS
US-09-160-119-2
                                       LENGTH: 447
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       SEQ ID NO 4
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GAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFN-----PQRRYNPSSHVLSGACAGAVAA 276
                                                                                                                                        63 LQASRQILQEEGPTAFWKGHVPAQILSIGYGAVQFLSF-----EMLTELVHRGSVYDA 115
                                     ---NSH-IANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSP--YHRVTDCVRAVWQNEGA 221
                                                                     116 REFSVHFVCGGLAACMATL----TVHPVDVLRTRFAAQGEPKVYNTLRHAVGTMYRSEGP 171
                                                                                                                                                                                     277 AATTPLDVCKTLLNT --- QESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shah, Purvi
APPLICANT: An-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TILLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incut-
Species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
ATTORNEY AGENT INFORMATION:
NAME: B1111ng9, Lucy J.
REGISTARTION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMUNICATION:
TELECOMUNICATION INFORMATION:
TELECHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09234613
Patent No. 6132973
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
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TYPE: amino acid
STRANDEDNES: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                334 YQIPSTAIAWSVYEFF 349
                                                                                                                                                                                                                                                                                                    291 KAALSTGFMFFSYEFF 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LIBRARY: SPLNNOT02; CLONE: 207452
US-09-234-613-12
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
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                                                                                                                                                                         222 GAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFN-----PQRRYNPSSHVLSGACAGAVAA 276
                                                                                                                                                                                                                                                                                                                                                                                                        277 AATTPLDVCKTLLNT---QESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 DAAMNPAEVVKQRMQMYNS-PYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 MIYEFLQEHFNPQRRY----NPSSHVL--SGACAGAVAAAATTPLDVCKTLLNTQESLA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 YEALPAGATVTTHM--VAGAVAGILEHCVMYPIDCVKTRMQSLQ-----PDPAARYRNV 114
                                                                                                                                                    115 LEALWRIIRTEG----LWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG---- 167
                                                                                                                                                                                                                              ---NSH-IANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSP--YHRVTDCVRAVWQNEGA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 HWVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRN--VLEALWRIIRTEG---LWR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 PMRGLNVTATGAGPAHALYFACYEKLKKTL-SDV----IHPGGNSHIANGAAGCVATLLH 184
                                                                                                 295 OSSIYPMEVLKTRMALRKTGQYSGMLDCARRILAKEGVAAFYKGYIPNMLGIIPYAGIDL
                                        42;
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Fatent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Sleeman, Matthew
APPLICANT: Ornust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 1100.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
Score 259; DB 4; Length 320;
Pred. No. 2.1e-18;
62; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
13.2%; Score 255.5; DB 4;
Best Local Similarity 28.6%; Pred. No. 8.4e-18;
Matches 84; Conservative 51; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 YQIPSTAIAWSVYEFF 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 KAALSTGFMFFSYEFF 306
                     Similarity
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US-09-188-930-339
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 Query Match
Best Local Simi
Matches 78;
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LENGTH: 469
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APPLICANT: Gong, Weilong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 TEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV----IHPGGNSHIANGAAGC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 VATLLHDAAMNPAEVVKQRM-----QMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTT 230
    -----AHKYRNTWDCGLQILKKEGLKAFYKGTFPRLGRVC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 AGATVTTH----MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 SHGVLGLYRGLSSLLYGSIPKAAVRFGMFEFLSNHMRDAQGRLDSRRGLLCGLGAGVAEA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 VVVVC-----PMETVKVKFIHDQTSSNPKYRGFFHGVREIVR----EQGLKGTYQGLTA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 QLTMNVPFQAIHFMTYEFLQEHF----NPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.4%; Score 221; DB 2; Length 31: 25.1%; Pred. No. 1.6e-14; Live 46; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 593783ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33, Application US/08775009 Patent No. 5935783 GENERAL INFORMATION:
                                          337 PSTAIAWSVYEFFKYLITK 355
                                                                       288 LDVAIVFVIYDEVYKLLNK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.1:
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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    243 VIKTRMOGLE-
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                                                                                                                                   Sequence 32, Application US/08775009
Patent No. 5935783
GENERAL INFORMATION:
APPLICANT: Gong, Weilong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Branuel, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
TITLE OF INVENTION: Vellocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 ALPA-GATVTTH----MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALW 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 RIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANG---- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 OTVRSHGVLGLYRGLSSLLYGSIPKAAVRFGMFEFLSNHMRDA---QGRLDSTRGLLCGL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 AAGCVATLLHDAAMNPAEVVKQRM-----QMYNSPYHRVTDCVRAVWQNEGAGAFYR 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 SYTTQLTMNVPFQAIHFMTYEFLQEHF---NPQRRYNPSSHVLSGACAGAVAAATTPLD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 VCKTLLNTQESLALNSHITGHITGMASAFRTVYQVG-----GVTAYFRGVQARVIYQI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 GAPEVT-----MSSLFKQILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLK 461
297 LNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 311;
                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSE: No. 5935703ris, LLP STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/775,009 FILING DATE: J-DEC-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.8%; Score 229.5; DB 225.7%; Pred. No. 2.1e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CH-0681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTORNEY CAGENT INFORMATION:
APTORNEY CAGENT INFORMATION:
NAME: Trujilo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/POCKET NUMBER: CH-068
TELECOMMUNICATION INFORMATION:
TELEPAN: (215) 568-3100
TELEPAN: (215) 568-3100
TELEPAN: (215) 568-3100
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 311 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19103
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-775-009-32
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Best Local Similarity
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                                                                                                 RESULT 10
US-08-775-009-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .28 WRPMRGLNVTATGAGPAHALYFA-----CYEKLKKTLSDVIHPGGNSHIANG---AAGCV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 TGAMAVTCAQPTDVVKVRFQAMIRLGTGGERKYRGTWDAYRTIAREEGVRGLWKGTWPNI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 TMNVPFQAIHFMTYEFLQEHFNPQRRY--NPSSHVLSGACAGAVAAAATTPLDVCKTLLN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 ATLLHDAAMNPAEVVKQRMQMY-----NSPYHRVTDCVRAVWQNEGAGAFYRSYTTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.4%; Score 201.5; DB 2; 25.3%; Pred. No. 2.6e-12; ive 44; Mismatches 139;
                                                                                                                                                                                                                                                           APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Amaral, M. Catherine
APPLICANT: Amaral, M. Catherine
TITLE OF INVENTION: UCP3 Genes
TITLE OF INVENTION: UCP3 Genes
GORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENLISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
  242 -----MNAPLGRYRSPLHCMLKMVAQ-EGPTAFYKGF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/937,466
                                                                                                                                                                                                    Sequence 4, Application US/09172528
Patent No. 5952469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (660) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.3%
Matches 78; Conservative
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MOLECULE TYPE: peptide
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CLASSIFICATION:
                                                              349 FKYLITKR 356
                                                                                                    288 VTYEQLKR 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                               US-09-172-528-4
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288 LLNTQESLALNSHITGHITGMASAFRTVYQVG-----GVTAYFRGVQARVIYQIPSTA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --AHKYRNTLDCGVQILKNEGPKAFYKGTVPRLGRVCLDVA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 WRPMRGLNVTATGAGPAHALYFA-----CYEKLKKTLSDVIHPGGNSHIANG---AAGCV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 RSPYSGL-----VAGLHRQMSFASIRIGLYDSVKQFYT-----PKGADHSSVAIRILAGCT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 ATLIHDAAMNPAEVVKQRMQMY-----NSPYHRVTDCVRAVWQNEGAGAFYRSYTTQL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TMNVPFQAIHFMTYEFLQEHFNPQRRY -- NPSSHVLSGACAGAVAAAATTPLDVCKTLLN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 TVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA---RYRNVLEALWRIIRTEGL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 TQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPS--TAIAWSVYEF 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.4%; Score 201.5; DB 2; Length 43 25.3%; Pred. No. 2.6e-12; tive 44; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Chang, Ning
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
SITRET: 75 DENISE DRIVE
CITY: HILLSDRONGH
STATE: CALIFORNIA
                                                                                                                                                                                                                       Sequence 4, Application US/08937466
Patent No. 5846779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-(
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4341
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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amino acid
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Matches 78; Conservative
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292 IVFVIYDEVVKLLNK 306
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                                                                               341 IAWSVYEFFKYLITK 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
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                                     247 RMQGLE---
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                                                                                                                                                                                                  US-08-937-466-4
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291 TQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPS--TAIAWSVYEF 348
                                                                                  242 -----WINAPLGRYRSPLHCMLKMVAQ-EGPTAFYKGF------VPSFLRLGAWNVMMF 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 RSPYSGL----VAGLHROMSFASIRIGLYDSVKQFYT----PKGADHSSVAIRILAGCT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 TGAMAVTCAQPTDVVKVRFQAMIRLGTGGERKYRGTMDAYRTIAREEGVRGLWKGTWPNI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 WRPMRGLNVTATGAGPAHALYFA-----CYEKLKKTLSDVIHPGGNSHIANG---AAGCV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 TVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA---RYRNVLEALWRIIRTEGL 127
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,579
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hes 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.4%; Score 201.5; 25.3%; Pred. No. 2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
FILING DATE:
                                                                                                                                                                                                                                                                                     ; Sequence 4, Application US/09503579
; Patent No. 6248561
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TO TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 432 amino acids TYPE: amino acid
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les 78; Conserv
                                                                                                                                             349 FKYLITKR 356
                                                                                                                                                                                        288 VTYEQLKR 295
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US-09-503-579-4
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                       291 TQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPS--TAIAWSVYEF 348
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                                                             242 -----WNAPLGRYRSPLHCMLKMVAQ-EGPTAFYKGF-----VPSFLRLGAWNVMMF 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
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Pred. No. 2.6e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/318,199
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES:
CORRESONDENCES:
ADDRESSEE. SCIENCE & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
                                                                                                                                                                                                                                                   Sequence 4, Application US/09318199
Patent No. 6025469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 25.3%
Matches 78; Conservative
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STRANDEDNESS: si
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                                                                                                                                             288 VTYEQLKR 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94010
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Search completed: August 27, 2002, 03:58:49 Job time: 4891 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 27, 2002, 02:35:14 ; Search time 80.04 Seconds (without alignments) 436.988 Million cell updates/sec Run on:

US-09-870-113-2 1940 1 MELEGRGAGGVAGGPAAGPG......VYEFFKYLITKRQEEWRAGK 364 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	hypothetical prote		ice	mtRNA splice defec	hetical	Q	hypothetical prote	-	_	_	probable carrier p	hypothetical prote		S	Btl protein precur	PET8 protein - yea	probable carrier p	probable mitochond	probable carrier p		υ	~	mitochondrial solu	probable membrane	probable mitochond		citrate transporte	hypothetical prote	_
		GI .	T26089	T39149	S13533	S55179	A86205	T00582	S54524	G96770	T19322	T43493	S54495	T20290	T09362	S60949	JQ1459	S45458	S57116	T40968	S44092	T48156	T50686	T05350	T01729	S57544	T50393	T37576	G01789	018	S48451
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		Length	312	303	304	314	781	331	368	367	328	351	902	269	330	307	436	284	322	338	384	309	475	392	352	326	335	345	311	336	373
œ	Query	Match	41.2	31.0	28.8	28.6		26.1	16.2	15.3	15.2	15.1	٠	14.1	14.1	14.0	13.7	13.7	12.9	12.9	12.9	12.7	12.4	12.4	12.3	12.1	12.1		•	11.8	11.8
		Score	799	601	558.5	555.5	521	202	313.5	297	295	293	282.5	274	274	272.5	266.5	265.5	250.5	250	249.5	245.5	240.5	240	239.5	m	234.5	230.5	229.5	228.5	228
	Result	No.	1	7	٣	4	5	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

RESULT

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T32897 S64589	T22688 T50990	149871 T38879 B96830	A46595 T40033 S62485	H88567 S67662	T29640 B96753 T16533
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650 366	347	305 302 296	311 277 271	312	330 349 702
11.6	11.6	11.5	11.4 11.3 11.3	11.3	11.2
226 225.5	224.5	222.5 221.5	221 220 219	217.5	216.5 215
30 31 32	2 W W C	36 37	38 39 40	442	44 44 45

ALIGNMENTS

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A;Cross-references: EMBL:249408; NID:91008337; PID:91008338; MIPS:YJL133w
R;Katsoulou, C.; Tzermia, M.; Tavernarakis, N.; Alexandraki, D.
Yeast 12, 787-797, 1996
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A; Residues: 1-314 <KAW>
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N.Alternate names: protein YRR052c

C. Species: Saccharomyces cerevisiae

C. Date: 16 Sep-1992 #sequence_revision 16 Sep-1992 #text_change 21-Jul-2000

C. Accession: 513533; 538126

R. Wiesenberger, G.: Link, T.A.; von Ahsen, U.; Waldherr, M.; Schweyen, R.J.

J. Mol. Biol. 217, 23-37, 1991

A; Reference number: 813532; MUID:91108815

A; Rocession: 513533

A; Molecule type: DNA

A; Residues: 1-304 < AND

A; Cross-references: EMBL:X56444; NID:93995; PIDN:CAA39828.1; PID:93996

R; Vissers, S.; Urrestarazu, L.A.; Jauniaux, J.C.

submitted to the Protein Sequence Database, March 1994

A; Reference number: 538118

A; Molecule type: DNA

A; Reference number: 538126

    fission yeast (Schizosacchan

                                                                          Chacesion: T39149
Rioliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
Submitted to the EMBL Data Library, September 1997
A; Reference number: 221748
A; Accession: T39149
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Rossidues: 1-303 < OLI>
A; Resperimental Source: EMBL: 299168; PIDN: CAB16300.1; GSPDB: GN00066; SPDB: SPAC8C9.12c
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
probable RNA splicing proteinmitochondial carrier protein - fission yeast (S
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 DYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 IRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 SSTEGVYSLWRGISSVIMGAGPSHAIYFSVLEFFKSK----INASPDRPLASALAGACAI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 HFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHI 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 DYEGLPIGSPMYAHLLAGAFSGILEHSVMYPVDAIKTRMQMLNGVSRSVSGNIVNSVIKI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1304 <VIS>
A; Cross-references: EMBL:228277; NID:9486506; PID:9486507; MIPS:YKR052c
A; Experimental source: strain S288C
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 LLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 VRKCKGSLDVVRFIYNYGGIPSFFKGIRPRMVVAMPATAVSWAAYEAGKEILIR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 TGHITGMASAFRIVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.0%; Score 601; DB 2; 39.5%; Pred. No. 2.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD:S0001760; MIPS:YKR052c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 39.5%
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: SPDB:SPAC8C9.12c
A,Map position: 1
C,Superfamily: ADP,ATP c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 11R
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mtRNA splice defect-suppressing mitochondrial carrier MRS3 - yeast (Saccharomyces cer M;Alternate names: protein J0675; protein YJL133w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000
C;Accession: S5179; S01267; S20228; S56915; S71664
R;Katsoulou, C.; Tzermia, M.; Alexamdraki, D.
Submitted to the EMBL Data Library, May 1995
A;Description: The complete sequence of a 40.7 kb segment located on the left arm of yeast hypothetical proteins.
A;Reference number: S55159
A;Accession: S55179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sedneuc
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A.Residues: 1-86,'S',88-102,'L',104-127,'Y',129-141,'M',143-187,'R',189-314 <SCH>
A.Residues: 1-86,'S',88-102,'L',104-127,'Y',129-141,'M',143-187,'R',189-314 <SCH>
A.Residues: 1-86,'S',88-102,'L',104-127,'Y',129-141,'M',143-187,'R',189-314 <SCH>
B.Wiesenberger, G.; Link, T.A.; von Ahsen, U.; Waldherr, M.; Schweyen, R.J.
J. Mol. Biol. 27, 23-37, 1991
A.Title: MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new A.Reference number: S13532; MUID:91108815
A.Reference number: S13532; MUID:91108815
A.Residues: 19-314 <AWIE>
A.Residues: 19-34 <AWIE>
A.Reference number: S56425; NID:93992; PIDN:CAA39830.1; PID:93994
A.Reference number: S56912
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Reywords: duplication; mitochondrion; transmembrane protein P:20-109/Domain: ADP,ATP carrier protein repeat homology <ACP1> F:17-201/Domain: ADP,ATP carrier protein repeat homology <ACP2> F:206-301/Domain: ADP,ATP carrier protein repeat homology <ACP2> F:206-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                        5
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A;Cross-references: EMBL:X87371; NID:g854542; PID:g854563
A;Cross-references: EMBL:X87371; NID:g854542; PID:g854563
B;Schmidt, C.; Soellner, T.; Schweyen, R.J.
Mol. Gen. Genet. 210, 145-152, 1987
A;Title: Nuclear suppression of a mitochondrial RNA splice defect: nucleotide A;Reference number: S01267; MUID:88121698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 IRTEGLWRPMKGLNVTATGAGPAHALYPACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 DYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 STMEGSMALWKGVQSVILGAGPAHAVYFGTYEFCKARLISPEDMQTHQPMKTALSGTIAT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 LLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 HFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 TGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 MKDANIFGRASRAILEVHGWKGFWRGLKPRIVANIPATAISWTAYECAKHFLMK 303
                                                                                                                                                                                                                                                                                           Length 304;
                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                       28.8%; Score 558.5; DB 2;
40.1%; Pred. No. 6e-37;
tive 53; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 118; Conserv
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E

8

Length 781;

Indels

44; Mismatches 123; Score 521; DB 2; Pred. No. 1.9e-33;

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A;Residues: 1-781 <STO>
A;Cross-references: GB:AE005172; NID:g8954043; PIDN:AAF82217.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 AVTTPLDVVKTQLQCQCVCGCDRFTSSSI---SHVLRTIVKKDGYRGLLRGWLPRMLFHA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 PVRQDPD-----SGPDY--EALPAGATVTTHWVAGAVAGILEHCVMYPIDCVKTRMQSLQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277 AATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 PGG--NSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFYRSYTTQLTMNVPFQAIHFMTYEFLQE----HFNPQRRYNPSS----HVLSGACAGAVAA
                                                                                                                                                                                                                                                                              26.9%;
39.4%;
                                                                                                                                                                                                                                                                              Query Match 26.9%
Best Local Similarity 39.4%
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 PAAAICWSTYEGVLY 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86205
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.R.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719
A;Accession: A86205
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                          Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Function:
A;Description: probably involved in splicing of all intron for COB gene; essential
                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X87371; NID:9854542; PIDN:CAA60822.1; PID:9854563 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat home C;Keywords: mitochondrial inner membrane; mitochondrion; pre-mRNA splicing F;30-119/Domain: ADP,ATP carrier protein repeat homology AQCP1-5:127-211/Domain: ADP,ATP carrier protein repeat homology AQCP2-F;127-311/Domain: ADP,ATP carrier protein repeat homology AACP3-F;216-311/Domain: ADP,ATP carrier protein repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 ANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 314;
                                                                                                                                       A;Accession: S71664
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.6%; Score 555.5; DB 2; Length 39.1%; Pred. No. 1.1e-36; Live 50; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGD:S0003669; MIPS:YJL133w
                                                                                                        A; Reference number: S71643; MUID: 96408771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 39.18
Matches 118; Conservative
                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-314 <KAF>
                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: SGD:MRS3
A,Cross-references:
A,Map position: 10L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Genome: nuclear
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probable mitochondrial carrier protein [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein T27E13.10 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Decie: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001 C;Accession: T00582; C84705 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K submitted to the EMBL Data Library, May 1998 A;Bescription: Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Accession: Tunner.

A.Accession: Tunner.

A.Accession: Tunner.

A.Status: translated from GB/EMBL/DDBJ

A.Status: translated from GB/EMBL/DDBJ

A.M. Status: translated from GB/EMBL/DDBJ

A.R. Status: translated from GB/EMBL/DDBJ

A.R. Status: 1-33 - (ROU)

A.R. Status: The Mathemator (R.S.) - (ROU)

A.R. Status: A
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Pred. No. 8.2e-33;
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A;Introns: 263/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP
C;Keywords: mitochondrion
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39.78;
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hypothetical protein F1017.9 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Restence number: A86141; MuID:21016719
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <STO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005173; NID:g6939230; PIDN:AAF31732.1; GSPDB:GN00141
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
293 SNKSYSVTHPHVTNGRPAALSNSISLSLRTVYQSEGVLGFFSGVGPRFVWTSVQSSIMLL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 GAVAGILEHCVMYPIDCVKTRMQS-LQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 LLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYE 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 ATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQR 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 VTGSLATGATYFGFIESTKKWIEE-SHPSLAGHWAHFIAGAVGDTLGSFIYVPCEVIKQR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 MQMYNSP------YHRVTDCVRA---VWQNEGAGAFYRSYTTQLTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 NVPFQAIHFMTYEFLQEHFN-----PQRRYNPS-SHVLSGACAGAVAAAATTPLDVCKT
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28.7%; Pred. No. 4.7e-16;
ive 51; Mismatches 129; Indels
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R;Lloyd, C.
submitted to the EMBL Data Library, November 1994
A;Reference number: 219108
A;Accession: T19322
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Best Local Similarity
Matches 87; Conserv
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353 LYQ 355
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                                             345 VYE 347
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A;Cross-references: GB:249705; EMBL:Z49700; NID:g825556; PIDN:CAA89802.1; PID:g825571; A;Experimental source: strain AB972 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein YMR166c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM8520.15c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 29-oct-1999
C;Accession: S54524; S54611
R;Hurt, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54510
                                                                                                                                                                                                                                                            PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPG 166
                                                                                                                                                                  225 YRSYTTQLTMNVPFQAIHFMTY-----EFLQEH-FNPQRRYNPSSHVLSGACAGAVA 275
                                                                                                                                                                                                                                                                                                                                                                                                                  276 AAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQ 335
                                                                                                                                                                                                                                                                                                                                                                                                                                            PVRQDPDSGPDYEALPAGATVTT----HMVAGAVAGILEHCVMYPIDCVKTRMQSLQPD 106
                                                                                                                                                                                                                                  G--NSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAF 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 KQRMQM---YNSP-----YHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFM 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 TYE-FLOEHFNPORR-----YNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLAL 297
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                       28;
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Best Local Similarity '29.0%; Pred. No. 2.3e-17;
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Mismatches 119;
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43;
Conservative
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125;
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Matches
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86; Conservative
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Best Local Similarity
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           A Molecule Type: DNA
A, Residues: 1-328 <WILL>
A, Residues: 1-328 <WILL>
A, Cross-references: EMBL: Z46787; PIDN: CAA86739.1; GSPDB: GN00021; CESP: C16C10.1
A, Experimental source: clone C16C10
C; Genetics: CESP: C16C10.1
A, Map position: 3
A; Introns: 22/1; 125/2; 179/1; 298/1
C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
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6
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Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                         77 VAGAVAGILEHCVMYPIDCVKTRMQSLQP----DPAARYRNVLEALWRIIRTEGLWRPMR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 GLSPTMVMALPATVFYFTTYDNLSVWLKKKMCCRRAFSPEKWTPPDWS--AAAVAGIVAR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 --IRIGGSIDDMNKSITTVIKDMYHSRGISAFSSGLVPRLVKVSPSCAIMISFYEYFKFL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                   ---HPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----RYRNVLEALWRIIRTEG---LWRPMRGLNVT 137
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                              3 SPCES-------GKTINCSGAPSSSCVIPLDVVKIRLQQQTRP----FPKGECFYYH- 48
                                                                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                                                                    22 SPGESALLDGWLQRGVGRGAGGGEAGACRPP----VRQDPDSGPDYEALPAGATVTTHM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                   154 TIAVTVVSPIEMIRTKMQSKRLTYHEIGHLVRSSMATKGISSFYLGWTPTMLRDIPFSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HFMTYEFLQEHFNPQRRYNPSSH-----VLSGACAGAVAAAATTPLDVCKTLLNTQESLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 LNSHITGHITGMASAFRTV----YQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYL
                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Hono sapiens (man)
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 2
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 2
C; Accession: T43493
A; Reference number: Z22516
A; Reference number: Z22516
A; Reference number: Z25516
A; Residues: 1-351 < AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 351;
                                                                                                                                                                                                                 Length 328
                                                                                                                                                                                                             ; Score 295; DB 2; Length 32; Pred. No. 5.8e-16; 48; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 PAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AL133584
A:Experimental source: adult testis; clone DKFZp434C119
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.1%; Score 293; DB 2; L 25.1%; Pred. No. 9.2e-16; iive 50; Mismatches 140;
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                             133 GLNVTATGAGPAHALYFACYEKLKKTLSDVI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein DKFZp434C119.1 - human
                                                                                                                                                                                                               Query Match 15.2%;
Best Local Similarity 27.8%;
Matches 101; Conservative 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
Note: DKFZp434C119.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 FQK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches
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probable carrier protein YPR021c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein YP9367.01c
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 22-Oct-1999
C.Accession: S54495
R.Baddock, K.; Churcher, C.M.
Submitted to the EMBL Data Library, May 1995
A; Reference number: S54059
A; Reference number: S54059
A; Residues: 1-902 - RBAD
C; Genetics: A; Map position: 16 R
A; Map position: 16 R
C; Superfamily: probable carrier protein repeat homology <ACPI>C; Reywords: duplication; transmembrane protein
C; Keywords: duplication; transmembrane protein
F; 527-615/Domain: ADP, ATP carrier protein repeat homology <ACPI>F; 521-711/Pomain: ADP, ATP carrier protein repeat homology <ACPI>F; 724-814/Domain: ADP, ATP carrier protein repeat homology ACPI>F; 724-814/Domain: ADP, ATP carrier protein repeat A
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8
CLLYCNGVLEPLYLCPNGARCATWPQDPTRFTGTMDAFVKIVRHEGTRTLM---SGLPAT 122
                                                                                                                                                                                                                                                                                                                                         251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 HFN---PQRRYNPSSHVLSGACAGAVAAAATTPLDVCKT----LLNTQESLALNSHITGH 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAGPAHALYFACYEKLKKTLSD-----VIHPGGNSHIANGAAGCVATLLHDAAMNPAEV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQE---HFNP----QRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSH 300
                                                                                                                                                                                                EVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 WLNGLRPKDQTSVGMSFVAGGISGTVAAVLTLPFDVVKTQRQVALGAMEAVRVNPL---H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 VKQRMQMYNSPY----HRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 ITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQEE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 902;
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29.4%; Pred. No. 2.1e-14;
iive 45; Mismatches 129
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A;Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome A;Reference number: S71713; MUID:96437977
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A.Note: YORR22W
C.Superfamily: ADP.ATP carrier protein; ADP.ATP carrier protein repeat homology
C.Superfamily: ADP.ATP carrier protein; transmembrane protein
C.Keywords: duplication; mitochondrion; transmembrane protein
C.Keywords: duplication; motochondrion; trapeat homology <ACPI>
F.9107_Domain: ADP.ATP carrier protein repeat homology <ACPI>
F.208-300/Domain: ADP.ATP carrier protein repeat homology <ACPI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S71724
A;Molecule type: DNA
A;Residues: 1-307 <GAW>
A;Cross-references: EMBL:X92441; NID:g1050762; PIDN:CAA63185.1; PID:g1050774
C;Genetics:
        245 TYEFLQEHFN--PQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHIT 302
                                                                                                                                                                                                       ----A 260
                                                                                                                --IRVPTEVVKQRMQ--TGQFTSAPSAVRMIASKEGFRGLYAGYRSFLLRDLPFDAIQFC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 RPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 VAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA------RYRNVLEALWRIIRTEGLW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 307;
                                                                                                                                                                                   208 IYEQLCLGYKKAARRELSDPENALIGAFAGALTGAVTTPLDVIKTRLMVQGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.0%; Score 272.5; DB 2; 27.2%; Pred. No. 3.3e-14; tive 54; Mismatches 130;
                                                                                                                                                                                                                                                303 GHITGMASAFRTVYQVGGVTAYFR 326
                                                                                                                                                                                                                                                                           261 KQYQGIVDCVQTIVREEGAPALLK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 81; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F23K16.90 - Arabidopsis thaliana (S.Species: Arabidopsis thaliana (mouse-ear cress) (S.Species: Arabidopsis thaliana (mouse-ear cress) (S.Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-oct-1999 (S.Accession: T09362 (S.Evan M.) MITPhy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4
A:Introns: 19/1: 56/1; 85/1; 109/2; 139/3; 157/3; 189/3; 219/3; 237/1; 257/3; 284/3
                                                                                                                                                                                                                                                                                                             A;Map position: 4
A;Introns: 53/2; 174/3; 226/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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                                                                                                           A; Reference number: Z19253
A; Accession: T20290
A; Accession: T20290
A; Accession: Preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-269 <WILL>
A; Cross-references: EMBL: Z68160; PIDN: CAA92291.1; GSPDB: GN00022; CESP: D1046.3
A; Experimental source: clone D1046
C; Genetics:
Species: Caenorhabditis elegans
Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 17-Mar-2000
Accession: T20290
Matthews, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 TVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 MRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 AEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQ 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 RAVANKKESGRCSPLEGAACGSVAGFIAAGLTTPLDVAKTRIMLTKN------GPAPG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 EHFNPQR----RYNPSSHVLSGACAGAVAAATTPLDVCKTLLNTQESLALNSHITGHITG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 IVITHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAAR--YRNVLEALWRIIRTEGLW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 RPMRGLNVTATGAGPAHALYFACYE----KLKKTLSDVIHPGGNSHIANGAAGCVATLLH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GFIAAGGFKDI 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
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A;Experimental source: cultivar Columbia; BAC clone F23K16
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.1%; Score 274; DB 2; Length 330; ilarity 33.0%; Pred. No. 2.8e-14; Conservative 29; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 ILSTLKEVYTSNGVRGLYSGVVPRVMWISGGGFVFFGAYETAMHFTKFL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 MASAFRIVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYE----FFKYL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 TLFEGFIAGGTAGVVVETALYPIDTIKTRLQ-----AARGGGKIVLKGLY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128;
                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 274; DB 2;
; Pred. No. 2.1e-14;
49; Mismatches 128
                                                                     R;Matthews, P. submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.1%;
27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 27.08
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: T09362
A; Molecule type: DNA
A; Residues: 1-330 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: ATSP:F23K16.90
                                                                                                                                                                                                                                                                                        A; Gene: CESP: D1046.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87;
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Best Local (
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Search completed: August 27, 2002, 03:57:40 Job time: 4946 sec

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Risullivan, T.D.; Strelow, L.I.; Illingworth, C.A.; Phillips, R.L.; Nelson Jr., O.E. Plant Cell 3, 1337-1348, 1991
A;Title: Analysis of maize brittle-1 alleles and a defective suppressor-mutator-induced A; Reference number: J01459; MUID: 93005685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Zea mays (maize)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Sep-1999
C;Accession: JQ1459
197 V-----RNSMPVAKTKGQKTRNDLIAGAIGGTVGTMLNTPFDVVKSRIQSVD--AVS 246
                                                                                                189 NPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHF-MTYE 247
                                                                                                                                                              137 VPFELIKIRMQDVKSSYLGPMDCLKKTIKNEGIMGLYKGIESTMWRNALWNGGYFGVIYQ 196
                                                                                                                                                                                                                                248 FLQEHFNPQRRYNP-----SSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 TTHMVAGAVAGILEHCVMYPIDCVKTRMQ--SLQPDPAARYRNVLEALWRIIRTEGLWRP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L----CTYPMELIKTRVTIEKDVYDNVAHAFVKILRDEGPSELYRGLTPSLIGVVPYAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| || |: : | | | : : | 301 NFYAYETLKRLYRRATGRRPGADVGPVATLLIGSAAGAIASSATFPLEVARKQMQ---- 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSH-----IANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 FRGNAVNVLRVAPSKAIEHFTYDTAKKFLT----PKGDEPPKIPIPTPLVAGALAGFAST 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFMTYEFLQEHF-----NPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLINTQESL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 ALNSHITGHITGMASAFRTVYQ------VGGVTAYFRGVQARVIYQIPSTAI 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 -----VGAVGG-----RQVYQNVLHAIYCILKKEGAGGL---YRGLGPSCIKLMPAAGI 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 PG-RSPGESALLDGWLQRGVGRGAGGGEAGACR----PPVRQDPDSGPDYEALPAGATV 72
                                                                                                                                                                                                                                                                                                                                                               299 SHITGHITGMASAFRIVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVY----EFFKYL 352
                                                                                                                                                                                                                                                                                                                                                                                                         247 SAVKKYNWCLPSLL-VIYREEGFRALYKGFVPKVCRLAPGGSLMLVVFTGMMNFFRDL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M79333; NID:g168425; PIDN:AAA33438.1; PID:g168426 C;Comment: This protein acts as an adenylate translocator in amyloplasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alfutrons: 206/3; 260/3
Alfutrons: 206/3; 260/3
Alfutrons: 206/3; 260/3
Alfutrons: 206/3; 260/3
C.Superfamily: Btl protein; ADP,ATP carrier protein repeat homology C.Superfamily: Btl protein $F1-75,Domain: transit peptide (amyloplast) *status predicted <TNP>F:76-436/Product: Btl protein *status predicted <AMPT>F:76-436/Product: Btl protein *status predicted <AMPT>F:131-217/Domain: ADP,ATP carrier protein repeat homology <ACPI>F:226-312/Domain: ADP,ATP carrier protein repeat homology <ACPI>F:236-313/Domain: ADP,ATP carrier protein repeat homology <ACPI>F:323-413/Domain: ADP,ATP carrier protein repeat homology <ACPI>F:327-347/Domain: transmembrane *status predicted <TML>
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Best Local Similarity 25.9
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JQ1459
A; Molecule type: mRNA
A; Residues: 1-436 <SUL>
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 27, 2002, 03:56:08; Search time 37.5 Seconds (without alignments) 375.838 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-870-113-2 1940 1 MELEGRGAGGVAGCPAAGPG......VYEFFKYLITKRQEEWRAGK 364

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 Total number of hits satisfying chosen parameters:

105224 seqs, 38719550 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P23500 saccharomyc		Q03829 saccharomyc	Q09461 caenorhabdi	Q9bzj4 homo sapien		Q9qxx4 mus musculu	P29518 zea mays (m	P38921 saccharomyc	OgujsO homo sapien	Q9va73 drosophila		sacch	Q9h2d1 homo sapien	рошо	homo	mus m	Q10442 schizosacch	P53007 homo sapien	P40556 saccharomyc	Q9bqt8 homo sapien		P39953 saccharomyc		Q20799 caenorhabdi	043772 homo sapien		P32089 rattus norv	Q09834 schizosacch	Q9wvd5 mus musculu	P34519 caenorhabdi	75	021153 caenorhabdi
SUMMARIES	ΙD	MRS4 YEAST	MRS3_YEAST	YM39_YEAST	YQ51_CAEEL	CG69_HUMAN	ODC2_YEAST	CMC2_MOUSE	BT1_MAIZE	PET8_YEAST	CMC2_HUMAN	CMC1_DROME	DNC_HUMAN	SFC1_YEAST	MFT_HUMAN	SA18_HUMAN	CMC1_HUMAN	SA18_MOUSE	YDE9_SCHPO	TXTP_HUMAN	YIA6_YEAST	ODC_HUMAN	YG5F_YEAST	YEA6_YEAST	TXTP_BOVIN	CMC2_CAEEL	MCAT_HUMAN	YD1K_SCHPO	TXTP_RAT	YAD8_SCHPO	ORT1_MOUSE	TXTP_CAEEL	MCAT_RAT	CMC1_CAEEL
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	Score	558.5	555.5	313.5	295	289	272.5	268	266.5	265.5	265	261.5	259	250.5	244.5	240	240	235	230.5	229.5	228	227	225.5	225	224.5	224.5	\sim	222.5	221	219	219	219	215.5	215
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Q9bxi2 homo sapien Q19529 caenorhabdi	P40035 saccharomyc P23641 saccharomyc					P38127 saccharomyc	-
ORT2_HUMAN CMC3_CAEEL	YEO3_YEAST MPCP_YEAST	ORT1_YEAST	PM34_HUMAN	PM34_MOUSE TXTP_YEAST	UCP1_HUMAN	RIM2_YEAST	UCP3_CANFA
			· ·		Н	7	-
301	300	308	307	307 299	307	377	311
10.9	10.7	10.4	10.4	10.3	10.1	10.1	10.0
211.5	207	201.5	201	200 197.5	196.5	195.5	194.5
34 35	36 37	38	40	41	43	44	45

ALIGNMENTS

MES4_YEAST MES4_YEAST MES4_YEAST MES4_YEAST MES4_YEAST MES4_YEAST D1_NOV-1991 (Rel. 20, Created) D1_NOV-1991 (Rel. 20, Last annotation update) Mitochondrial RNA splicing protein MSR4. Mitochondrial RNA splicing protein MSR4. MES4 OR YROSOZ. Saccharcomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomyc	PRT; 304 AA.	.ed) sequence update) annotation update) protein MSR4.	mros or innoze. Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBL_TaxID-4932;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-MA301; MEDLINE-91108815; PubMed*1703236; Wiesenberger G., Link T.A., von Ahsen U., Waldherr M., Schweyen R.J.; WRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new members of the mitcochondrial carrier family.";	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE S., Urrestarazu L.A., Jauniaux JC.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: MRS4 SUPPRESSES A MITOCHONDRIAL SPLICE DEFECT IN THE -!- FUNCTION: MRS4 SUPPRESSES A MITOCHONDRIAL SPLICE DEFECT IN THE FIRST INTRON OF THE COB GENE. IT MAY ACT AS A CARRIER, EXERTING ITS SUPPRESSOR ACTIVITY VIA MODULATION OF SOLUTE CONCENTRATIONS IN THE MITOCHONDRION (POSSIBLY OF CATIONS). NOT ESSENITAL. -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane. -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. STRONG, TO MILARITY: BEACH MAY BE ISOFORMS OF THE SAME CARRIER PROTEIN.	ight. It is produced to the bioinformatics and stitute. There are no ons as long as its contour temoved. Usage not reement (See http://wwb-sib.ch).	h_carrier. 3. ARRIER; 2. ane; Repeat; Transmembrane; Transport; BLOCK I (APPROXIMATE). HLOCK II (APPROXIMATE).
"1991 (Rel "1991 (Rel "1991 (Rel "1991 (Rel "1993	TANDARD;	20, Creat 20, Last 37, Last splicing	revisiae (Bake ; Ascomycota; s; Saccharomyc	A. : PubMed=17032 Link T.A., vo two suppressor of the mitocho 7:23-37(1991).	tarazu L.A., 994) to the EM 984) to the EM 54 SUPPRESSES OF THE COB GE DR ACTIVITY VI PRION (POSSIBL CCATION: Intele. BELONGS TO THE 81 BOTH PROTEI	nntry is copyrss Institute of informatics In instituti is statement is a license agt to license@is	139828.1;
		01-NOV-1991 (Rel 01-NOV-1991 (Rel 01-NOV-1991 (Rel 15-DEC-1998 (Rel Mitochondrial RNA	Mast or innostr. Saccharomyces cer Eukaryota; Fungi, Saccharomycetales	SEQUENCE FROM N.2 SEQUENCE FROM N.2 STRAIN=#1301; MEDLINE=91108815; Wiesenberger G., "MRS3 and MRS4, i are new members or J. Mol. Biol. 21;	ENCE FROM N.2 ers S., Urres litted (MAR-1) FIRST INTRON ITS SUPPRESSO THE MITCOHON SUBCELLULAR I Inner membrar SIMICARITY: I TO YEAST MRS?	WISS-PROT en the Swis ropean Bioin y non-proi ed and this es requires d an email	EMBL; X56444; CAREMBL; Z28277; CAAPTR; S13535; S135355; S13535; S13535; S13535; S13535; S13535; S13535; S13535

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt C., Soellner T., Schweyen R.J.;
"Nuclear suppression of a mitochondrial RNA splice defect: nucleotide
sequence and disruption of the MS3 gene.";
Mol. Gen. Genet. 210:145-152(1987).
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                         62 DYEALPAGATVITHMVAGAVAGILEHCVMYPIDCVKTRMOSLQPDPAARYRNVLEALWRI 121
                                                                                                                                                                                                                                122 IRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                 182 LLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAI 241
                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                          Yeast 12:787-797(1996).
                                                                                                                                                                                                                                                                                                                                                242 HFWTYEFLOEHFNPORRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHI
                                                                                                                                                                                                                                                                                                                                                                 MRS3 OR YJLJ33W OR J0675. Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                         302 TGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFRYLITK 355
                                                                                                                                                                                                                                                                                                                                                                                                                         250 MKDANTFGRASRAILEVHGWKGFWRGLKPRIVANIPATAISWTAYECAKHFLMK 303
                                                                                                                                                3;
                                                                                                                 Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288C / FY1679;
MEDLINE=9640871; PubMed=8813765;
Katsonlou C., Tzermia M., Tavernarakis N., Alexandraki D.;
Sequence analysis of a 40.7 kb segment from the left arm of chromosome X reveals 14 known genes and 13 new open reading fincluding homologues of genes clustered on the right arm of
                                                                                                                                              Indels
                                                        POTENTIAL.
5ABBF9858B547EDC CRC64;
                                                                                                                                             53; Mismatches 120;
                                                                                                                 DB 1;
                                                                                                                28.8%; Score 558.5; DB 40.1%; Pred. No. 3.7e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1989 (Rel. 11, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat.
Mitochondrial RNA splicing protein MRS3.
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MEDLINE-88121698; PubMed-2448588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91108815; Pubmed=1703236;
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                                                                       33307
                                                                                                                               Best Local Similarity 40.1%
Matches 118; Conservative
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102
139
194
228
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P10566;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 RNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHI 171
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                                                                                                                                                                                                                    inner membrane.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. STRONG,
TO YEAST MRS4; BOTH PROTEINS MAY BE ISOFORMS OF THE SAME CARRIER
FIRST INTRON OF THE COB GENE. IT MAY ACT AS A CARRIER, EXERTING ITS SUPPRESSOR ACTIVITY VIA MODILATION OF SOLUTE CONCENTRATIONS THE MITOCHONDRION (POSSIBLY OF CATIONS).
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 ANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
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BLOCK II (APPROXIMATE).
BLOCK III (APPROXIMATE)
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EMBL; X56445; CAA39830.1; ALT_INIT.
EMBL; X06239; CAA29582.1; ALT_SEQ.
EMBL; X06371; CAA60822.1; -.
EMBL; X97371; CAA60822.1; -.
EMBL; 249408; CAA89428.1; -.
PIR; S20228; S20228; S20228; S20238; S20238; S20338; S20388; S20338; S20338; S20338; S20338; S20338; S20338; S20388; S20388; S20388; S20388
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Best Local Similarity 39.18
Matches 118; Conservative
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YM39_YEAST

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353 ITK 355
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 7051_CAEEL
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                                                                                                                                                                 Lloyd C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KQRMQM---YNSP-----YHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFM 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 TYE-FLQEHFNPQRR-----YNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLAL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 VTA-TGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                           Hunt S., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (Potential).
-!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 NS-----HIT-GHITGMAS----AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWS
                                                                   YMR166C OR YM8520.15c.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.2%; Score 313.5; DB 1; Length 368; 29.0%; Pred. No. 1.1e-17;
                                                                                                                                                                                                                                                                                                                                                  SGD: S0004776; YMR166C.
InterPro: IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PROSTIE: PS00215; MITOCH_CARRIER; 2.
Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            B583100018DF045D CRC64;
                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Putative mitochondrial carrier YMR166C.
368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            40992 MW;
                                                                                                                                                                                                                                                                                                                                         EMBL; 249705; CAA89802.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
STANDARD;
                                                                                                                                       SEQUENCE FROM N.A. STRAIN=S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 VYE 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYQ 355
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YM39_YEAST
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 VAGAVAGILEHCVMYPIDCVKTRMQSLQP----DPAARYRNVLEALWRIIRTEGLWRPMR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 GLNVTATGAGPAHALYFACYEKLKKTLSDVI-------HPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 GLSPIMVMALPAIVFYFITYDNLSVWLKKKMCCRRAFSPEKWIPPDWS--AAAVAGIVAR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNSHITGHITGMASAFRTV----YQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:IRIGGSIDDMNKSITTVIKDMYHSRGISAFSSGLVPRLVKVSPSCAIMISFYEYFKFL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SPCES------GKTTNCSGAPSSCVTPLDVVKIRLQQQTRP----FPKGECFYYH- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 SPGESALLDGWLQRGVGRGAGGGEAGACRPP----VRQDPDSGPDYEALPAGATVTTHM 76
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 YWAGYDLFKT--NLQRRQGPDHNPFVVSFVSGAAAGVVASIFTHPFDVIKT--NCQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 LLHDAAMNPAEVVKORMOMYNSPYHRVTDCVRAVWONEGAGAFYRSYTTQLTMNVPFQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 HFMTYEFLQEHFNPQRRYNPSSH-----VLSGACAGAVAAAATTPLDVCKTLLNTQESLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WormPep; C16C10.1; CE01489.
InterPro; IPR01993; Mitoch_Carrier.
Paran; FP00153; Mito_Carrier.
PR051TE; PS000115; MITOCH, CARRIER; 1.
Hypothetical protein; Mitochondrion; Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 POTENTIAL.
36743 MW; EA1E9E329A764DF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.2%; Score 295; DB 1; 27.8%; Pred. No. 2.8e-16;
                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Putative mitochondrial carrier C16C10.1.
328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
   PRT;
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   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113
166
257
                                                                                                                                                                          C16C10.1.
Caenorhabditis elegans.
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Best Local Similarity
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146 1
237 2
328 AA;
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                  Rhabditidae; Pelc
NCBL_TaxID=6239;
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RESULT

RESULT 4 YQ51_CAEEL

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357 QEE 359
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099297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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ODC2_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamra Y., Isogai T., Sugano S., "NED human cDNA sequencing project." "NEDO human cDNA sequencing project." Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional prediction of the coding sequences of 79 new genes deduced by analysis of cDNA clones from human fetal liver."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- DOMAIN: COMPOSED OF THREE HOWOLOGOUS DOMAINS.
-1- ALTERNATIVE PRODUCTS: 2 1soforms; 1/CGI-69L (shown here) and 2; are produced by alternative splicing.
-1- TISSUE SPECIFICITY: Expressed in many tissues. Abundant in testis
                                                                                                                                                                                                                                                                    "Overexpression of the human 2-oxoglutarate carrier lowers mitochondrial membrane potential in HEK-293 cells: contrast with the unique cold-induced mitochondrial carrier CGI-69."; Blochem. J. 353:369-375(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Fetal liver;
Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; Tyowards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435(2001).
                                                                                             Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=20272150; PubMed=10810093;

Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;

Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";

Genome Res. 10:703-713(2000).
                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                        Yu X.X., Lewin D.A., Zhong A., Brush J., Schow P.W., Sherwood Pan G., Adams S.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
             CG69_HUMAN STANDARD; PRT; 359 AA.
C9B5J4; O9UF66; Q9Y379; O9P182;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial carrier protein CGI-69 (PRO2163).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 15-359 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21154917; PubMed=11230166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1). TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain, and Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inner membrane.
                                                                                                                                                                                                                         PubMed-11139402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                            TISSUE-Liver;
   CG69_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 -----RYRNVLEALWRIIRTEG---LWR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 PMRGLNVTATGAGPAHALYFACYEKLKKTL-----SDVIHPGGNSHIANGAAGCVATLL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 LNSHITGHITGMASAFRIVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PAGISPLOOMVASGTGAVVTSLFMTPLDVVKVRLOSQRPSMASELMPSSRLWSLSYTKLP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: ::| :| || || || 66 SSLQSTGKCLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHEGTRTLW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 HDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 TVTVISPLELMRTKLQAQHVSYRELGACVRTAVAQGGWRSLWLGWGPTALRDVPFSALYW
                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPSSLOSTG -> W (IN ISOFORM 2).
L -> F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G -> R (IN REF. 6).
952AA3DB5F5F9BD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 PAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.9%; Score 289; DB 1; 24.5%; Pred. No. 9.4e-16; Live 50; Mismatches 14C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_012756
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30-MAY-2000 (Rel. 39, Last sequence update)
001-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial 2-oxodicarboxylate carrier 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                 Polymorphism.
                                                                                                             EMBL, AF317711; AAG60687.1; --
EMBL, AF151827; AAD34064.1; --
EMBL, AR133584, CA863728.1; --
EMBL, AK026060; BAB15341.1; --
EMBL, BC001398; AAH01398.1; --
EMBL, BC009330; AAH0330.1; --
EMBL, AF119864; AAF69618.1; --
INTERPLO; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39214 MW;
                                                                                                                                                                                                                                                                                                                    PF00153; mito_carr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 24.59
les 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               splicing; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
235
279
338
72
72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 122
161
215
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64
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us-09-870-113-2.rsp

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CMC2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ′,
                                                                                                                                                                                                                                                                                               Walker J.E., "Identification in Saccharomyces cerevisiae of two isoforms of a novel mitochondrial transporter for 2-oxoadipate and 2-oxoglutarate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 VAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA-----RYRNVLEALWRIIRTEGLW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 RPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLYRGISSPMLMEAPKRATKFACNDQYQKIFKNLFNTNETTQKISIAAGASAGMTEAAVI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 NPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHF-MTYE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                               matrix to the cytosol where they are used in the biosynthesis of lysine and glutamate, respectively, and in lysine catabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 ISGAVAGISELTVMYPLDVVKTRFQLEVTTPTAAAVGKQVERYNGVIDCLKKIVKKEGFS 76
                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Transports C5-C7 oxidicarboxylates across the inner membranes of mitochondria. Can transport 2-oxoadipate, 2-oxoqiutarate, adipate, glutarate, 2-oxopimelate, oxaloacetate, citate and malate. The main physiological role is probably to supply 2-oxoadipate and 2-oxoglutarate from the mitochondrial
                                                                                                                                                                                                                                                                   PubMed=11013234;
Palmieri L., Agrimi G., Runswick M.J., Fearnley I.M., Palmieri F.,
                                                                                                    SECUENCE FROM N.A.

STAIN-S288C / FY1679;

MEDLINE=9643797; PubMed=8840505;

Galisson F., Dujon B.;

Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV of the yeast Saccharomyces cerevisiae.";
                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIMIS; PR00926; MITOCARRIER, PROSITE; PS00215; MITOCH_CARRIER; 3.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%; Score 272.5; DB 1; Length 307; 27.2%; Pred. No. 1.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4089082A64DBA97C CRC64;
                                                    Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Mismatches 130;
                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                    mitochondrial transporter for 2-ox
J. Biol. Chem. 276:1916-1922(2001)
-!- FUNCTION: Transports C5-C7 oxo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z75130; CAA99440.1; -. EMBL; X92441; CAA63185.1; -.
ODC2 OR YOR222W OR YOR50-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00153; mito_carr; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81; Conservative
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300
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280 3
307 AA;
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                                                                                                                                                                                                                                                CHARACTERIZATION.
                                                                     NCBI_TaxID=4932;
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Best Local S
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Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yammanka I.,
A alio T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
ARA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schrimi L., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Schrimi L., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Futuno M., Anon H., Baldarelli R., Barsh G.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Lyons P., Marchionni L., Mashima J., Wazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodiiguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Wynshay-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Wynshay-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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A FUNCTION IN THE UREA CYCLE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   090XX4; 09DCF5; 09CZF6; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier
                                                197 V-----RNSMPVAKTKGQKTRNDLIAGAIGGTVGTMLNTPFDVVKSRIQSVD--AVS 246
248 FLQEHFNPQRRYNP-----SSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INNER MEMBRANE (BY SIMILARITY).
-!- TISSUE SPECIFICITY: AT E10.45, EXPRESSED IN BRANCHIAL ARCHES AND LIREIMB AND TAIL BUDS. AT E13.5 EXPRESSION IS PREDOMINANT IN EPITHELIAL STRUCTURES AND THE FOREBRAIN, KIDNEY AND LIVER. EXPRESSION IN LIVER IS MAINTAINED INTO ADULTHOOD.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR
                                                                                                                                                                   299 SHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVY----EFFKYL 352
                                                                                                                                                                                                                    247 SAVKKYNWCLPSLL-VIYREEGFRALYKGEVPKVCRLAPGGSLMLVVFTGMMNFFRDL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sinasac D.S., Crackower M.A., Lee J.R., Kobayashi K., Saheki T., Scherer S.W., Tsul L.-C., "Genomic structure of the adult-onset type II citrullinemia gene, SLC25A13, and cloning and expression of its mouse homologue."; Genomics 62:289-292(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               676 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6J; TISSUE-Embryo, and Kidney; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. MEDLINE-20079163; Pubmed=10610724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25, member 13) (Citrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLC25A13 OR ARALAR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 MRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSH------IANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 -----VGAVGG-----RQVYQNVLHAIYCILKKEGAGGL---YRGLGPSCIKLMPAAGI 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 PG-RSPGESALLDGWLQRGVGRGAGGGEAGACR-----PPVRQDPDSGPDYEALPAGATV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| || |: : | | | : : | 301 NFYAYETLKRLYRRATGRRPGADVGPVATLLIGSAAGAIASSATFPLEVARKQMQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 ALNSHITGHITGMASAFRTVYQ------VGGVTAYFRGVQARVIYQIPSTAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 TTHMVAGAVAGILEHCVMYPIDCVKTRMQ--SLQPDPAARYRNVLEALWRIIRTEGLWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 FRGNAVNVLRVAPSKAIEHFTYDTAKKFLT----PKGDEPPKIPIPTPLVAGALAGFAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 LLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 HFMTYEFLQEHF-----NPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESL
                                                                                                              Suppressor mutator-induced mutable allele.";
Plant Cell 3:1337-1348(1991).
-!- FUNCTION: COULD PLAY A ROLE IN AMYLOPLAST MEMBRANE TRANSPORT.
-!- SUBCELLULAR LOCATION: CALIOROPLAST; amyloplast.
-!- TISSUE SPECIFICITY: ENDOSPERM OF DEVELOPING KERNELS.
-!- TISSUE SPECIFICITY: ENDOSPERM OF DEVELOPING KENNELS.
                                                         R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; irrovice; 3.
Print, PR00153; mito_carr; 3.
PRINT, PR00926; mitoCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
Transit peptide; Chloroplast; Amyloplast; Transmembrane.
Transit peptide; Chloroplast; Amyloplast; Transmembrane.
TRANSIT 1 75
BRITTLE-1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138; Indels
                                MEDLINE-93005685; PubMed-1668652;
Sullivan T.D., Strelow L.I., Illingworth C.A., Phillips
Nelson O.E. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9600C05F603E9DAE CRC64;
                                                                                                'Analysis of maize brittle-1 alleles and a defective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.7%; Score 266.5; DB 1
25.9%; Pred. No. 7.1e-14;
tive 57; Mismatches 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46627 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M79333; AAA33438.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 AWSVYEFFKYLITKROEE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 AFMCYEACKKILVDKEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JQ1459; JQ1459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 2
327 3
436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MaizeDB; 47578;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PET8_YEAST
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

Panicoideae; Andropogoneae; Zea.

NCBI_PAXID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 DAAMNPAEVVKORMOMYNSPYHRVIDCVR----AVWQNEGAGAFYRSYTTQLIMNVPFQA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TNPLEIVKIRLQVAG----EITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFSA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 NVTATGAGPAHALYFACYEKLKKTLSDVI-----HPGGNSHI-----ANGAAGCVATLLH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 IHFMTYEFLQEHF-NPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 GAVAGILEHCVMYPIDCVKTRMQSLQPDPA----ARYRNVLEALWRIRTEGLWRPMRGL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 LPQLLGVAPEKA-----IKLTVNDFVRDKFMHKDGSVPLLAEIFAGGCAGGSQVIF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 HITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : |: || : : || : : | 560 Y-----NGVTDCFRKILREEGPKALWKGVAARVFRSSPQFGVTLLTYELLQ 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAB28397).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN REF. 2; BAB28397)
S -> F (IN REF. 2; BAB22390).
5E3952F08E5E58C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%; Score 268; DB 1; Length 67 28.2%; Pred. No. 9.2e-14; Live 47; Mismatches 122; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALCIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Brittle-1 protein, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                           5 (POTENTIAL).
6 (POTENTIAL).
EF-HAND 1.
EF-HAND 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 AA
                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANCESTRAL (EF-HAND 4.
send an email to license@isb-sib.ch)
                                                                                                                                                                                                              PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00018; EF_HAND; FALSE_NEG.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                           MGD; MGI:1354721; Slc25a13.
InterPro; IPR002049; EF-hand.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                       EMBL; AK002829; BAB22390.1; -. EMBL; AK012670; BAB28397.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74466 MW;
                                                                                                                                                                       Pfam; PF00036; efhand; 3. Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 82; Conserv
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676 P
                                                                                                                                                                                                                                                                                                Calcium-binding
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P29518;
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TRANSMEM
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TRANSMEM
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DOMAIN
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16;

Gaps

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PRT;
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                                                                                                                                                                                                                                                                                                              family 25, member 13) (Citrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 345:725-732(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Genet. 22:159-163(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 252-675 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics 62:289-292(1999).
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding mitochondrial tissues.";
                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                         SLC25A13 OR ARALAR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALCIUM-BINDING.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606,
                                                                                                                                                                                                                                 CMC2_HUMAN
                                                                                                                                                                   226
                                                                                                                                                                                                                                               셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FKUM N.A.

STRAIN=5286C, FV1679;

MEDLINE=95076713; PubMed=7985421;

Werhasselt P., Aert R., Voet M., Volckaert G.;

Werhasselt P., Aert R., Voet M., Volckaert G.;

Worlbeolide sequence analysis of an 8887 bp region of the left arm of yeast chromosome XIV, encompassing the centromere sequence.";

Yeast 10:945-951(1994).

-! SUBCELULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (Potential).

-! DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

-! SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 VTATGAGPAHALYFACYE----KLKKTLSDVIHPGG-----NSHIANGAAGCVATLLHD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=GRF88;
MEDLINE=94005822; PubMed=8402262;
Lalo D., Stettler S., Mariotte S., Slonimski P.P., Thuriaux P.;
"Two yeast chromosomes are related by a fossil duplication of their
                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 284;
                                                                                                                                                                                                                                                                                   Lalo D., Stettler S., Mariotte S., Gendreau E., Thuriaux P., "Organization of the centromeric region of chromosome XIV in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                761378D67DAFD343 CRC64;
                                                                                                                                                                                                          C. R. Acad. Sci., III, Sci. Vie 316:367-373(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7%; Score 265.5; DB 1; 27.1%; Pred. No. 5.1e-14; tive 47; Mismatches 125;
          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
PETR OR YNLO03C OR N2012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                    MEDLINE=95028151; PubMed=7941739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31027 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U02536; AAA64802.1; -.
EMBL; X77114; CAA54377.1; -.
EMBL; Z71279; CAA95862.1; -.
PIR; S45120; S45120.
PIR; S45458; S45458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                       Keast 10:523-533(1994).
                                                                                                                                                                                                         centromeric regions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284 AA;
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                 NCBI_TaxID=4932;
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Kobayashi K., Sinasac D.S., Iijima M., Boright A.P., Begum L., Lee J.R., Yasuda T., Ikeda S., Hirano R., Terazono H., Crackower M.A., Kondo I., Tsul L.-C., Scherer S.W., Saheki T.;
"The gene mutated in adult-onset type II citrullinaemia encodes a putative mitochondrial carrier protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goela D., Hultman M., Scheet P., Cordes M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL SOLUTE CARRIER. MAY HAVE
A FUNCTION IN THE UREA CYCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PANCREAS, PLACENTA, HEART AND BRAIN.

-1- DISEABE: DEPECTS IN SLC25A13 ARE A CAUSE OF ADULT-ONSET TYPE-II
CITRULLINABMIA (CTLN2). CTLN2 IS CHARACTERIZED BY A LIYER SPECIFIC
DEFECT IN THE REGULATION OF ARGININOSUCCINATE SYNTHASE (ASS)
RESULTING IN A DEPECTENCY OF ASS. A FEW YEARS AFTER ONSET PATIENTS
ENTER A COMA AND SUFFER CEREBRAL EDEMA.
-1- MISCELLANEOUS: BINDS CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UJSO; Q9UNIT; Q9NZWI; O14566; O14575;
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2002 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier
SAVVASAPGASLEPISYDYMKVKSRPYISKLYSOGSEQLIDFTTHMLSSSIGEICACL-- 110
                                                                                                                                                                                                                                                                                                                                                             -! - TISSUE SPECIFICITY: HIGH LEVELS IN LIVER AND LOW LEVELS IN KIDNEY
                                                                                                                                                                                                                    111 -VRVPAEVVKQRTQVHSTNSSWQTLQSILRNDNKEGLRKNLYRGWSTTIMREIPFTCIQF 169
                                                                                                                                                                                                                                                                                                              244 MTYEFLQEHF---NPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                               AAMNPAEVVKQRMQMY - - NSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a second member of the subfamily of calcium-carriers expressed in human non-excitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 6-251 FROM N.A., AND DISEASE.
MEDLINE=20079163; PubMed=10610724;
Sinasac D.S., Crackower M.A., Lee J.R., Kobayashi K., Saheki T.,
Scherer S.W., Tsui L.C.;
"Genomic structure of the adult-onset type II citrullinemia gene,
SIC25A13, and cloning and expression of its mouse homologue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 ITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                675 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. MEDLINE-99295931; PubMed-10369257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Del Arco A., Agudo M., Satrustegui J.;
"Characterization of a second member of
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300 HITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFK 350
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                                                                                                                                                                                                                                                              cissues.
                                                         RESULT 11
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                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                              between the Swiss Institute of Bioinformatics and the EMBL outstatine Buropean Bloinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 LPQLLGVAPEKA-----IKLTVNDFVRDKFMHKDGSVPLAAEILAGGCAGGSQVIF- 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TNPLEIVKIRLQVAG----EITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFSA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 IHFMTYEFLQEHF-NPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 GAVAGILEHCVMYPIDCVKTRMQSLQPDPA----ARYRNVLEALWRIIRTEGLWRPMRGL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 NVTATGAGPAHALYFACYEKLKKTLSDVI-----HPGGN-----SHIANGAAGCVATLLH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%; Score 265; DB 1; Length 675;
28.2%; Pred. No. 1.6e-13;
Live 47; Mismatches 122; Indels 40; Gaps
 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 DAAMNPAEVVKQRMQMYNSPYHRVTDCVR----AVWQNEGAGAFYRSYTTQLTMNVPFQA
                                                                                                                                                                                                                                               InterPro; IRR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF001036; efhand; 3.
Pfam; PF001036; efhand; 3.
PRINTS; PR00926; MITOCRRIER.
PROSITE; PS00018; EF_HAND; FALSE_NEG.
PROSITE; PS00118; MITOCH_CARRIER; 3.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                  SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                         5 (POTENTIAL).
6 (POTENTIAL).
EF-HAND 1.
EF-HAND 2.
ANCESTRAL CALCIUM SITE 3.
EF-HAND 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q -> QQ (IN REF. 4).
M -> T (IN REF. 2).
AD07EDBC6C68989B CRC64;
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                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                 EMBL; AF118838; AAD38501.1; -.
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                                                                                                                           CAB62206
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532
675 AA;
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MIM; 605814;
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Best Local Simi
Matches 82;
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TRANSMEM
TRANSMEM
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CA_BIND
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REPEAT
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EMBL;
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RA MEDINE-ZOUGOUS, Pubmed-al0/3118.2;

RA Adams M.D., Celnighter S.E., Lip P.W., Hoskins R.A., Gocayne J.D.,

RA Adams M.D., Celnighter S.E., Lip P.W., Hoskins R.A., Galle R.E.,

B. Sutton G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,

RA MIN K.H., Doyle C. Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballaw R.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Ballaw R.M., Basu A., Baxandale J., Bayraktaroglu L., Beasley E.M.,

Ballaw R.M., Cawley B.W., Berman B.P., Bhandari D., Bolshakov S.,

Buttis K.C., Bucchan M.R., Bouck J., Baycaktaroglu L., Beasley E.M.,

RA Burtis K.C., Bucchan M.R., Bouck J., Baycaktaroglu L., Bolshakov S.,

RA Buttis K.C., Buchan M.R., Bouck J., Baycaktaroglu L., Dietz S.M.,

Buttis K.C., Buchan M.R., Bouck J., Baycaktaroglu L., Bolshakov S.,

RA Buttis K.C., Buchan D.A., Bulller H., Cadieu E., Center A., Chandra I.,

RA Buttis K.C., Buchan M.R., Bouck J., Baycakter P., Brutis R.A.,

Cader M., Gong F., Gorrell J.H., Cadieu E., Center A., Chandra I.,

RA Bosler C., Gabrielista C.C., Ferraz C., Ferriac S., Boukov B.C., Dunn P.,

RA Bosler C., Gabrielista C.C., Ferraz C., Ferriac S., Boukov B.C., Dann P.,

RA Bosler C., Gabrielista C.C., Ferraz C., Ferriac S., Kulp D., Laiz Z.,

Alali M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A.,

Alali M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Mattei B., McInton K.A., Li J.J., Harrandez J.R., Mocheco D.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Woller B., McInton K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Rabazzolo M., Pittann G.S., Pan S., Pollard J., Wolley M., Murphy L.,

Rabazzolo M., Pittann G.S., Pan S., Pollard J., Wolley M., Murphy R., Murphy L., Muzny D.M., Nelson D.R.,

Rabazzolo M., Pittann G.S., Pan S., Pollard J., Wolley R., McHort K., Wassarman D.A., Weilson D., Yang S., Zhu K., Woodage T., Singson M., Stupski M., Woodage T., Singson M., Stupski M., Woodage T., Singson M., Stupski M., Walley S.W., Rollon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Trācheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20115110; PubMed-10642534;
Del Arco A., Agudo M., Satrustegui J.;
Characterization of a second member of the subfamily of calcium-binding mitochondrial carriers expressed in human non-excitable
: :| : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                               CMC1_DROME STANDARD; PRT; 695 AA. 694A73; 09VA73; 09VA72; 09VA74; 09U5V8; 16-0C7-2001 (Rel. 40, created) 16-0C7-2001 (Rel. 40, Last sequence update) 16-0C7-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcium-binding mitochondrial carrier Aralari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
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513 YFPTYAHTKAMMADKDGYNHPLTLLAAGAIAGVPAASLVTPADVIKTRL---QVVARSGQ 569
                                                             301 ITCHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYL
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                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 VTATGAGPAHALYFACYEKLKKTLSDVIH------PGGNSHIANGAAGCVATLLHD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --TNPLEIVKIRLQVAGEIASGSKIRAWSVVREL----GLFGLYKGARACLLRDVPFSAI 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 AAMNPAEVVKQRMQ----MYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HFMTYEFLQEHFNPQRRYN-PSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSH 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                          INNER MEMBRANE (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 3 ISOPORMS; 1 (SHOWN HERE), 2 AND 3; MAY BRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR
  SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 PQLMGVAPEKA-----IKLTVNDLVRDKLTDKKGNIPTWAEVLAGGCAGASQVVF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHIPFPFNWIPTLPVARCOE -> LTKSLPN (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
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                                                                                                                                        SUBFAMILY.
-!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> A (IN REF. 1).
-> L (IN REF. 1).
8EC93D92031F5B77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANCESTRAL CALCIUM SITE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN ISOFORM 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> AP (IN REF. 1).
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; Pred. No. 3.1e-13;
41; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (POTENTIAL).
2 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Problem | Property |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBG70028646; araiari.
InterPro; IPR002048; EF-hand.
InterPro; IPR001993; Mit_carrier.
InterPro; IPR001993; Mitoh_carrier.
Pfam; PF00153; efhand; 3.
PRINTS; PR00155; mito_carr; 3.
PRINTS; SN00054; EFh; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, Y18197; CAB62169.1; -.
EMBL; AE003774; AAF57048.1; -.
EMBL; AE003774; AAF57049.1; -.
EMBL; AE003774; AAF57050.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76753 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.5%;
29.5%;
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653
695 AA;
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CONFLICT
SEQUENCE
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Responsible for the uptake of deoxynucleotides into the matrix of the mitochondria. Transports all four deoxy NDPs, and, less efficiently, the corresponding dNTPs. Does not transport dNNPs, NMPs, deoxynucleosides, nucleosides, purines, or pyrimidines. Supply deoxynucleotides to the mitochondrial matrix for conversion to triphosphates and incorporation into mitochondrial DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- DISBASE: Likely to be medically important by providing the means of uptake into mitochondria of nucleoside analogs, leading to the mitochondrial impairment that underlies the toxic side effects of such drugs in the treatment of viral illnesses, including AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dolce V., Fiermonte G., Runswick M.J., Palmierl F., Walker J.E.; "The human mitochondrial deoxynuclectide carrier and its role in the toxicity of nucleoside antivirals."; Proc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- TISSUE SPECIFICITY: Expressed in all tissues examined except for placenta. Highest levels in colon, kidney, lung, testis, spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                             01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and in cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
570 TT--YTGVWDATKKIMAEEGPRAFWKGTAARVFRSSPQFGVTLVTYELLQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Renard S., Mondesert G., Besnard F.;
"MUP 1, a mitochondrial uncoupling protein.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ251857; CAC27560.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ301616; CAC37793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF182404; AAG16903.1;
BC001075; AAH01075.1;
BC005120; AAH05120.1;
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            protein 1).
SLC25A19 OR DNC OR MUP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
PubMed=11226231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE=Lung;
                                                                                                                                                                                          DNC_HUMAN
Q9HC21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                      DNC_HUMAN
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us-09-870-113-2.rsp

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                                                                                      -:- FUNCTION: Transports cytoplasmic succinate, derived from isocitrate by the action of isocitrate lyase in the cytosol, into the mitochondrial matrix in exchange for funarate.
-:- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.
-:- INDUCTION: BY ETHANOL OR ACETATE AS SOLE CARBON SOURCES. REPRESSED BY GLUCOSE.
                   "Identification of the yeast ACR1 gene product as a succinate-fumarate transporter essential for growth on ethanol or acetate."; FEBS Lett. 417:114-118(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VREHLENLGIFKKNDTPKPKPLK -> RKGAFQKIWVYSRR MTHQSQSH (IN REF. 1).
EC29718a0F5011A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 ATLIHDAAMNPAEVVKQRMQ------MYNSPYHRVTDCVRAVWQNEGAGAFYR 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 HWVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNV-------LEALWRIIR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 TEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL----SDVIHPGGNSHIANGAAGCV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 EAVL---VVNPMEVVKIRLQAQHLTPSEPNAGPKYNNAIHAAYTIVK----EEGVSALYR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 GVSLTAARQATNOGANFTVYSKLKEFLQNYH--OMDVLPSWETSCIGLISGAIGPFSNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVG------GVTAYFRGVQARVIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYTTQLTMNVPFQAIHFMTY - - - - EFLQEHFNPQRRYNPSSHV - LSGACAGAVAAAATTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.9%; Score 250.5; DB 1; Length 322; 26.3%; Pred. No. 9.1e-13;
                                                                                                                                                                                                                                     DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial folate transporter/carrier.
MFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, 225485; CAA80973.1; -.
EMBL, 249595; CAA89624.1; -.
PIR, S36407; S36407.
PIR, S42280; S43280.
SGD; S0003856; SFC1.
InterPro: IPR001993; Mitoch_carrier.
Pfan; PP00175; Mitoch_carrier.
PROSITE; PS00215; MITOCH_CARRIER; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 AA; 35340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 LDTIKTRLOKDKSISLEKO--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 QIPSTAIAWSVYEFFK 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |: ::|||: :
286 VAPGQAVTFTVYEYVR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Q9H2D1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATTPLDVCKTLLNT---QESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                          63 YEALPAGATVTTHM--VAGAVAGILEHCVMYPIDCVKTRMQSLQ-----PDDPARYRNV 114
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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MEDLINE-98055465; PubMed-9395087;
Palmieri L., Lasorsa F.M., De Palma A., Palmieri F., Runswick M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
SEQUELINE-94203187; PubMed-7908717;
Fernandez M., Fernandez E., Rodicio R.;
"ACRI, a gene encoding a protein related to mitochondrial carriers, is essential for acetyl-CoA synthetase activity in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAFYRSYTTQLTMNVPFQAIHFWTYEFLQEHFN-----PQRRYNPSSHVLSGACAGAVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---NSH-IANGAAGCVATLIHDAAMNPAEVVKQRMQMYNSP--YHRVTDCVRAVWQNEGA
                                                                                                                    Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                                                                 13.4%; Score 259; DB 1; Length 320; 24.7%; Pred. No. 1.9e-13;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Succinate/fumarate mitochondrial transporter (Regulator of
                                                                                                                                                                                                                                                                                                                                                                             Mismatches 134; Indels
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Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                            57CE0F01D538B1BE CRC64;
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                   InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mitOcarr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
IPR001993; Mitoch_carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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SFC1 OR ACR1 OR YJR095W OR J1921
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                                                                                                                                                                                                                                                              35511 MW;
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193
313
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293
320 AA;
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hes 78; Conserv
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                                                                                                            Mitochondrion;
TRANSMEM 19
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P33303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                   Cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | || || || 11 || || 11 || 12 || 13 || 14 || 14 || 14 || 14 || 14 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 15 || 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 YQVVRARLQDQHMF-----YSGVIDVITKTWRKEGVGGFYKGIAPNLIRVTPACCI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGATVTTH-----MVAGAVAGILEHCVMYPIDCVKTRMQ-----SLQPDPAARYRNVLEA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 LDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAI 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 AWSTVFRHVRYENLIAGVSGGVLSNLALHPLDLVKIRFAVSDGLELRP----KYNGILHC 68
                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 AGCVATLLHDAAMNPAEVVKQRMQM----YNSP---YHRVTDCVRAVWQNEGAGAFYRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 YTTQLTMNVPFQAIHFMTYEFLQ----EHFN--PQRRYNPSSHVLSGACAGAVAAATTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                of a human gene encoding the carrier for entry of folates into mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 315;
                                                                                                                                                                                                                                                                                                                                                                          -- TISSUE SPECIFICITY: Ubiquitous.
-- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                             J. Biol. Chem. 275:36811-36817(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.6%; Score 244.5; DB 1; Length 3. 24.8%; Pred. No. 2.7e-12; tive 54; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60EBC0D61951EB6E CRC64;
                                                                                                                                                                                                                                                                                                                                                        -! - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
                                                                                                                                                         Titus S.A., Moran R.G.; "Retrovirally mediated complementation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                          SEQUENCE FROM N.A. MEDLINE-20538421; PubMed=10978331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 3
315 AA;
                                                                                                                                                                                                                                                                                             mitochondria.
                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Analysis of the cat eye syndrome critical region in humans and the region of conserved synteny in mice: a search for candidate genes at or near the human chromosome 22 pericentromere.", Genome Res. 11:1053-1070(2001).

-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 YRGAAVNLTLVTPEKAIKLAANDFFRRLL---MEDGMQRNLKMEMLAGCGAGMCQVVVTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 FYRSYTTQLTMNVPFQAIHFWTYEFLQE-HFNPQRRYNPSSH-VLSGACAGAVAAAATTP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inner membrane; Repeat; Transmembrane; Transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 315;
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25.2%; Pred. No. 6e-12;
ive 53; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B23A9E5036671634 CRC64;
                                   Last sequence update)
Last annotation update)
25, member 18.
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=21275466; PubMed=11381032;
         Created)
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ΜΣ
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Best Local Similarity 25.23
Matches 77; Conservative
01-MAR-2002 (Rel. 41, C1
01-MAR-2002 (Rel. 41, L6
01-MAR-2002 (Rel. 41, L6
Solute carrier family 2:
SLC25A18.
                                                                                                                                                             Homo sapiens (Human)
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225
288
315 AA;
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315 AA.

PRT;

STANDARD;

SA18_HUMAN

RESULT 15 SA18_HUMAN ID SA18_H

341 IAWSVY 346 || || || 297 IAQGVY 302 Qy Dp

Search completed: August 27, 2002, 04:16:45 Job time: 1237 sec

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Human polypeptide
Human uncoupling p
Human transport pr
Human protein SEQ
Human mitochondria
Novel human secret
Human polypeptide
Human bone marrow
Human ONEX ORF2730
Human ORFX ORF2734
Drosophila melanog
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| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseqy-embl/AA1981.DAT:*
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1036
1 MELEGRGAGGVAGGPAAGPG......GAAGCVATLLHDAAMNPAEG
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        747574 seqs, 111073796 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                       August 27, 2002, 03:55:57
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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624
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	A. A. A. This cytostatic; generathy; central nervous Huntington's disease Y-Drager Syndrome; ch screening; arthritis;
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ABB51123 AAG22077 AAG22078 AAG43093 AAG43093 AAG43094 AAG4206 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM42096 AAM50398 AAM50398 AAM503999 AAM503999999999999999999999999999999999999	H € . ≝∀'C
A A A A A A A A A A A A A A A A A A A	318 . 318 .
216222222222222222222222222222222222222	in; yy) No saupt saupt 16; 16; 16; 16; 191.
1122 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	tandard; Protein; 3 (first entry) peptide SE0 ID NO 6 tropic; immunosuppr mervous system; ne nervous system; ne n
www.444410000000000000000000000000000000	. a aireo a dependence
	0 96.0 0 1
24232 2223 2213 2211 2211 2211 2211 244 255 267 267 267 267 267 267 267 267 267 267	1 11505 11505 11505 11505 11505 110, no 110, n
111111111020202020202020202020202020202	RESULT AAM41505 AAM41505 AAM41505 XX
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AAB60113 AAM79039 AAB60658 AAU29748 AAM39719 AAM0938 AAB42966 AAB42980 AAB42980

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06-APR-2000;
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18-AUG-1999;
28-OCT-1999;
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                                                           18-AUG-1999;
12-NOV-1999;
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                                    09-APR-1999;
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                                                                                                                      Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB60113;
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3662-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system as released and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; uncoupling protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cardiant; vasotropic; cerebroprotective; neuroprotective, antibacterial; ophralmological; gastrointestinal; nephrotropic; gynaecological; vulnerary; thrombolytic; ene therapy; cancer; wound; infectious disease; thrombosis; arthritis;
                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang
                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                   Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                        Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                               75.9%; Score 786; DB 22;
100.0%; Pred. No. 1.3e-70;
ive 0; Mismatches 0;
                     Asundi V, Chen R, Ma Y,
Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                             Example 2; SEQ ID NO 6436; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNSHIANGAAGCVATLLHDAAMNPAE 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 146; Conservative
                                                                      2001-442253/47.
                      Liu C, A
Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                              318 AA;
(HYSE-) HYSEQ INC.
                                                                                   N-PSDB; AA160661
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                                                                                                                                                                                                                                                                                                                                                     specification.
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                      Tang YT,
                                             Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The present sequence is a human uncoupling protein. The nucleotide sequences encoding the uncoupling proteins may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Uncoupling proteins and nucleic acid sequences encoding them, useful for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 VTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
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100.0%; Pred. No. 2.1e-54;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 323-324; 343pp; English.
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                                                                                                                                                                                                                                                                     Ni J, Komatsoulis G,
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                                                       99US-0128701.
99US-0142821.
99US-0149448.
99US-0164751.
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99US-0148177.
99US-0149357.
99US-0162287.
                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
2000WO-US09534
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Matches 117; Conservative
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N-PSDB; AAC90457.
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cencer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: RECORDS for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PDYEALPAGATYTTHWVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 60
                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human mitochondrial solute carrier protein; hMSC-o; hypothalamus; preparation; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.9%; Score 516.5; DB 22; Length 299; 55.7%; Pred. No. 1.3e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Mismatches
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     Goodrich
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Yang Y, Wejhrman T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 AA;
                                                                                   N-PSDB; AAK52172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sim.
Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CN1269409-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB60658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB60658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
     NAME OF COLOR OF A PART OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences for 43 movel human transport proteins (designated TPPPs). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; hmwunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Υ;
                                                                                                                                                                                                                                          Isolated polypeptide with a human transport protein sequence is useful for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular systems -
                                                                                   ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Μa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 VTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Cao Y,
Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 289;
                                                                                 , Bandman O,
Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou P, Xu
F, Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 624; DB 22;
Pred. No. 2.1e-54;
                                                                                 Tang YT,
                                                                                                          Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.2%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Asundi V,
Wang J, Zhang J, Ren
                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 133-134; 165pp; English
                                                                           Hillman JL,
                                                                                                          Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM79039 standard; Protein; 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0496914.
2000US-056075.
2000US-059075.
2000US-063935.
200US-0654936.
2000US-063351.
2000US-063325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein SEQ ID NO 1701.
                           (INCY -) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders such as cancer
                                                                                                          Azimzai Y,
                                                                                                                                                         WPI; 2001-041424/05.
N-PSDB; AAF27733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C, E
Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157190-A2.
                                                                                 Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39-AUG-2001
                                                                                                       Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM79039;
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AAM79039 RESULT

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically the proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to home as the contractions to require the polypeptides and cells genetically cherapy, and can be used as nutritional supplements. They may be used to home as the cell proliferation; to regulate hematopoises;
                                                                                                                                                                                                                      bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias, AMUS9510-AMU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
                                                                                                                                                                                                                                                                                                                                                                                                                      1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 melr---sgsv--gsgavarrmdgds-----rdgggg------kdatgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 677;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                    47.0%; Score 486.5; DB 253.1%; Pred. No. 3.6e-40; ive 20; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 2864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM39719 standard; Protein; 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0488725.
2000US-055317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.1;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||||| ||||||
tllhdavmnpae 177
                                                                                                                                                                                                                                                                                                       677 AA;
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukaemia.
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                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                             The invention relates to a novel human mitochondrial solute carrier protein, hMSC-0 (AAB60658), and cDNA encoding it (AAF59920). hMSC-0 is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-0 proteins and nucleic acids, and the detection of hMSC-0 proteins and nucleic acids, and the sequence represents hMSC-0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 VKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                      95
                                                                                                                                                                                                                                                                                                                                                                                                                                    3 gdsrdgggg-----kdatgsedyenlptsasvsthmtagamagilehsvmypvds 52
                                                                                                    New human mitochondrion solute carrier protein and its nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                     GVGRGAGGGEAGACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDC
                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                     Length 331;
                                                                                                                                                                                                                                                                                                                                                                      32; Indels
                                                                                                                                                                                                                                                                                                                                   49.7%; Score 515; DB 22;
61.8%; Pred. No. 2.1e-43;
iive 18; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 KKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU29748 standard; Protein; 677 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 189; 765pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted protein #239.
                                                                                                                                   Claim 4; Page 20; 21pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
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                    Ħ
                                                                                                                                                                                                                                                                                                                                                                    97; Conservative
                    Gao X, Xiao
                                                  WPI; 2001-050544/07.
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                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                   N-PSDB; AAF59920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200179449-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2001
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                   Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU29748;
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT,
                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                   36
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19-OCT-2000;
30-NOV-2000;
                                                                                                                                               Wang
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                                                                                                                                               Ren F, Wa
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                    Ford JE,
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                                                                                                                                                                                      The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as latchiner's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed
                                                        Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 TRMOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antivral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                      Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 477; DB 22; Length 268;
Pred. No. 1e-39;
0; Mismatches 5; Indels
                                                      Qian XB,
Yang Y,
                                                      hen R, Ma Y, C
Xu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 TLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                    Example 4; SEQ ID NO 2864; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow protein, SEQ ID NO: 414.
                                                      Chen R,
                                                                   Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM00938 standard; Protein; 366 AA.
                                                     Liu C, Asundi V, Che
Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                    46.0%;
94.7%;
 19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-2000; 2000WO-US34960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                WPI; 2001-442253/47.
N-PSDB; AAI58875.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                    268 AA;
                                                                                                                                                                                                                                                                                                                                        C.N.S disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200153453-A2.
                                                                                                                                                                                                                                                                                                                                                              specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
                                                      Tang YT,
Wang J,
                                                                             Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM00938;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM00938
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The present sequence is one of 251 novel human polypeptides encoded by a bone marrow-expressed polynucleotide. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation infection, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 TTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 GLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                                                                      Υ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                  YT, Liu C, Asundi V, Chen R, Ma 1
', Xu C, Xue AJ, Yang Y, Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.9%; Score 465; DB 22; Length 366; 70.0%; Pred. No. 2.4e-38; ive 16; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ORFX ORF2730 polypeptide sequence SEQ ID NO:5460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 504-505; 648pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB42966 standard; Protein; 155 AA.
                                                                                                                                                                                                                                                                                                                                                                               ang J, Werhman T, X
Zhou P, Drmanac RT;
2000us-0552317.
2000us-0598042.
2000us-0620312.
2000us-063450.
2000us-063450.
2000us-0693036.
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                                                                                                                                                                                                                                                                                                                                                             Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.03
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488707/53.
                                                                                                                                                                                                                                                                                                                                                      Boyle BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 AA;
                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH90057
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
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us-09-870-113-4.rag

AAB42980 standard; Protein; 272 AA.

AAB42980

(first entry)

08-FEB-2001

AAB42980;

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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; antiannostimulant; cardant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinfiammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                    cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autocimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthitis, graft vs host disease, cardiovascular disease, diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 4641; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                         thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimkets RA, Leach M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                                                                 WO200058473-A2.
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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4;
                                                                                                                                                                                                                          61 PDYEALPAGATVTTHWVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWR 120
                                                                                                                                                                                                                                                                   93
                                                                                                                                         1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGGGGAGACRPPVRQDPDSG 60
                                                                                                                                                                               1 melr---sgsv--gsgavarrmdgds-----rdgggg------kdatgs 33
                                                                                                                                                                                                                                                                   34 edyenlptsasvsthmtagamagilehsvmypvdsvktrmgslspdpkagytsiygalkk
                                                                                                27;
                                                                                                                                                                                                                                                                                                           121 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANG 174
                                                                                                                                                                                                                                                                                                                               DB 21; Length 155;
                                                                                                    Indels
                                                                                                                                                                                                                                               36;
                                                         42.5%; Score 440.5; DB 2
52.3%; Pred. No. 2.5e-36;
Live 20; Mismatches 36
                                                                                                    Conservative
                                                                                 Similarity
Sequence 155 AA;
                                                         Query Match
Best Local Simi
Matches 91;
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; cationalisatic; antiparkinsonian; nootropic; neuroprotective; cospathic; anticonvulsant; thrombolytic; cosqulant; vasotropic; antiplabetic; hypotensive; dermatological; immunosuppressive; antiplamentory; antibacterial; antiviral; antifungal; antirheumatic; antiplidamentory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating to pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovasular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, auttoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                            Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; antiantional anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antifilammatory; antitivated is antibatocarial; antidiagal; antifrheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; ALDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemodlobininia; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                       bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acids and peptides derived from open reading frame \mathbf{X}, \mathbf{I} for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for treating e.g. cancers, proliferative disorde
neurodegenerative disorders and cardiovascular disease
                                                                                    Human ORFX ORF2744 polypeptide sequence SEQ ID NO:5488.
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99US-0127636.
99US-0127728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2000; 2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombosis; contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI: 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200058473-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1999;
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05-APR-1999;
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DYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMOSLQPDPAARYRNVLEALWRI 121
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                                                                                                                                                                                                                                                                    ABB51123;
                                                                                                                                                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01860-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                96 VKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKL 155
                                                                                                     Gaps
                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID NO 10182; 21pp + Sequence Listing; English.
                                                                          Length 272;
coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 10182
                                                                                                     17;
                                                                          DB 21;
                                                                      35.0%; Score 363; DB 21; 67.0%; Pred. No. 2.9e-28; iive 15; Mismatches 17
                                                                                                                                                                                         156 KKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                          Myers EW;
                                                                                                                                                                                                                                                                                               ABB61130 standard; Protein; 379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231.
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                    Local Similarity 67.09
nes 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
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                             272 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001
                             Sequence
                                                                                                                                                                                                                                                                                                                            ABB61130;
                                                                          Query Match
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                                                                                                                                                                                                                                                                   RESULT 11
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Gaps

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41; Indels

28.5%; Score 295; DB 22; 47.3%; Pred. No. 2.9e-21; iive 22; Mismatches 41;

62; Conservative

Query Match Best Local Similarity Matches 62; Conserv

Length 379;

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ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted proteins (I) and polynucleotide (II) sequences. (I) and (II) have various activities based on the Lissues and cells the genes are expressed in. Example of these activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; immunostimulant; anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological; neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular; antiparkinsonian; antimicrobial; and vulnerary (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; antiinflammatory; immunostimulant; orfostaltant; vascular; anti-angiogenic; ophthalmological; neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary; antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lugus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing; Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis; corneal graft neovascularisation; diabetic retinopathy; regeneration; neurological disorder; Huntington's chorea; Alzheimer's disease; parkinson's disease; chromosome 8.
                                                                                                                                                       61
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prevention, diagnosis and treatment of immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), anglogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzhelmer's disease and Parkinson's diseases and/or for promoting wound healing, regeneration and/or chemotaxis, ABA883193 and ABBS0300 represent sequences used in the exemplification of
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                                                                                                                                                                                                                    23.3%; Score 241.5; DB 22; Length 126; 48.6%; Pred. No. 1.8e-16; ive 11; Mismatches 23; Indels 23;
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                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 24869.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Best Local Similarity 39.9%; Pred. No. 4e-14;
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                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                     RIB polypeptides (AAM17050-54) are encoded by cDNA clones (AAT68953-57) that exhibit differential expression in blackcurrant fruit during the ripening period of fruit development. RIB7 shows 62% similarity to yeast MRS4, a yeast microchondrial RNA splicing protein. RIB7 is expressed almost entirely in fruit. The promoter region (AAT68952) of the RIB7 gene can be used as a fruit-specific promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated promoters from blackcurrant fruit - used for driving fruit-specific expression of DNA sequences in transgenic blackcurrant and other non-climacteric fruit
                                                                                                                                                        21.5%; Score 223; DB 21; Length 331; 39.9%; Pred. No. 4e-14; Live 22; Mismatches 51; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blackcurrant; fruit-specific promoter; RIB7; transgenic plant.
                                                                                                                                                                                                                                                                                                    167 G--NSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                   Brennan RM, Taylor MA, Woodhead MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 35-36; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     AAW17054 standard; Protein; 289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blackcurrant RIB7 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribes nigrum strain Ben Alder
                                              9905-0161406.
9905-0161359.
9905-0161360.
9905-0161361.
9905-0161992.
9905-0161993.
 99US-0160981.
99US-0160989.
99US-0161404.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95GB-0022558
                                                                                                                                            Query Match
Best Local Similarity 39.22
Loca 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-281041/25.
N-PSDB; AAT68957.
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                            AAW17054;
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ID AAW1
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76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                             Gaps
                                                                                                     136 VTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
                                                              4 ;
                                  Length 289;
                                                             Indels
                                                              42;
                                  20.4%; Score 211; DB 18; 38.5%; Pred. No. 5.5e-13; Live 26; Mismatches 42;
                                  Query Match
Best Local Similarity 38.5%;
Matches 45; Conservative
289 AA;
 Sequence
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Search completed: August 27, 2002, 03:55:58 Job time: 4910 sec

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August 27, 2002, 03:58:49; Search time 48.11 Seconds (without alignments) 97.987 Million cell updates/sec
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1036
1 MELEGRGAGGVAGGPAAGPG......GAAGGVATLLHDAAMNPAEG 193
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     231628 seqs, 24425594 residues
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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1: /cggl_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 15, Appl	10,	12,	12,	19,	19,	32,	33,	4, 4	7	1,	33	4	4	4	4	7	7	7	7	8	7	6	142	9	ý	9
SUMMARIES	ID	US-09-068-140A-15	US-09-068-140A-10	US-08-933-750C-12	US-09-234-613-12	US-08-933-750C-19	US-09-234-613-19	US-08-775-009-32	US-08-775-009-33	US-09-160-119-4	US-09-160-119-2	PCT-US94-09799-1	US-09-188-930-339	US-08-937-466-4	US-09-172-528-4	US-09-318-199-4	US-09-503-579-4	US-08-937-466-2	US-09-172-528-2	US-09-318-199-2	US-09-503-579-2	US-08-937-263B-8	US-09-142-565-2	US-08-791-495-9	US-09-188-930-142	US-08-937-466-6	US-09-172-528-6	US-09-318-199-6
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dР	Query	20.5	20.4	13.1	13.1	12.6	12.6	12.0	11.6	11.1	11.1	10.9	10.3	6.6	6.6	o.	6.6	9.5	9.5	9.5	9.5	9.4	9.1	9.1	9.1	0.6	9.0	0.6
	Score	212	211	135.5	135.5	131	131	124.5	120	115	115	112.5	106.5	102.5	102.5	102.5	102.5	98.5	98.5	98.5	98.5	97	94.5	94	94	'n	93.5	93.5
	Result No.	1	7	m	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27

; TOPOLOGY: unknown ; TOPOLOGY: unknown ; MOLECULE TYPE: peptide ; HYPOTHETICAL: YES ; ANTI-SENSE: NO ; FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ; ORGANISM: Ribes nigrum ; STRAIN: Ben Alder US-09-068-140A-15

15:

TELEX:
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: unknown

Sequence 6, Appli Sequence 56, Appl Sequence 56, Appl Sequence 56, Appl Sequence 51, Appl		4 4 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 105, App
US-09-503-579-6 US-08-807-861A-56 US-09-210-681-56 US-08-946-719A-56 US-08-518-878B-51	US-08-807-861A-51 US-08-470-868A-51 US-09-210-681-51 US-08-946-719A-51	US-08-209-747-4 US-08-458-298-4 US-08-518-878B-56 US-08-510-868A-56	US-07-609-716-41 US-08-475-411A-41 US-08-478-029A-41 US-07-609-716-105
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93.5 92.5 92.5	922.5 922.5 92.55	88888 99999999999999999999999999999999	88.5 88.5 87.5
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ALIGNMENTS

RESULT	ULT 1
-Sn	US-09-068-140A-15
	Sequence 15, Application US/09068140A
	GENERAL INFORMATION:
٠.	APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
٠.	APPLICANT: and Rex Michael Brennan
٠.	
٠.	NUMBER OF SEQUENCES: 15
••	CORRESPONDENCE ADDRESS:
٠.	ADDRESSEE: SmithKline Beecham Corporation
٠.	
٠.	×
٠.	STATE: PA
	COUNTRY: USA
•	ZIP: 19406-0939
	COMPUTER READABLE FORM:
	MEDIUM TYPE: Floppy disk
•-	COMPUTER: IBM PC compatible
•~	OPERATING SYSTEM: PC-DOS/MS-DOS
٠.	SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
٠.	CURRENT APPLICATION DATA:
••	APPLICATION NUMBER: US/09/068,140A
٠.	FILING DATE:
٠.	CLASSIFICATION:
٠.	
٠.	APPLICATION NUMBER: PCT/EP96/04807
	FILING DATE: No. 6281409ember 4, 1996
••	ATTORNEY/AGENT INFORMATION:
••	NAME: Dinner, Dara L.
•-	REGISTRATION NUMBER: 33,680
٠.	REFERENCE/DOCKET NUMBER: C70237
•-	TELECOMMUNICATION INFORMATION:
٠.	TELEPHONE: 610-270-5017
	TELEFAX: 610-270-5090

4; Gaps

Indels

42;

26; Mismatches

45; Conservative

Matches

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                                                                               61 PDYEALPA--GATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEAL 118
                                                                                                                                                                  119 WRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC 178
                                                                                                                                                                                        9
20.5%; Score 212; DB 4; Length 328; 35.8%; Pred. No. 3.2e-14; Live 27; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09068140A
Fatent No. 6281409
CENERAL INFORMATION:
APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
TITLE OF INVENTION: Blackcurrant Promoters and Genes
VMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: No. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 289 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                     Best_Local Similarity 35.89
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribes nigrum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                              ||: || : | :
|139 FATVASDAVITPMD 152
                                                                                                                                                                                                                                                      179 VATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN: Ben Alder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                               US-09-068-140A-10
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  Query Match
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Length 289;

Score 211; DB 4; Pred. No. 3.4e-14;

20.4%; 38.5%;

Query Match Best Local Similarity

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76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 YEALPAGATVTTHM--VAGAVAGILEHCVMYPIDCVKTRMQSLQ------PDPAARYRNV 114
                      136 VTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                           60 AMGLGAGPAHAVYFSVYEMCKETFS---HGDPSNSGAHAVSGVFATVASDAVITPMD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 320;
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Coejey, Neil J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OCMETATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%; Score 135.5; DB 2 llarity 28.8%; Pred. No. 2.7e-06; Conservative 26; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                        Sequence 12, Application US/08933750C
Patent No. 5932442
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lal, preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
MAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
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Matches 40; Conserv
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CLONE: 207452
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COUNTRY:
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63 LQASRQILQEEGPTAFWKGHVPAQILSIGYGAVQFLSF-----EMLTELVHRGSVYDA 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 CLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHEGTRTLM---SGLPAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 PAGISPLQQMVASGTGAVVTSLFMTPLDVVKVRLQSQRPSMASELMPSSRLWSLSYTKWK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 PAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA------
                                                                                                                                                                                                                                                                                                                                APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.6%; Score 131; DB 2; Best Local Similarity 24.9%; Pred. No. 9.1e-06; Matches 45; Conservative 19; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOES SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
                                                                                                                                                                                      Sequence 19, Application US/08933750C Patent No. 5932442 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                  APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer
APPLICANT: Bandman, Olga
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                                           168 ---NSH-IANGAAGCVATL 182
                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIBRARY: SYNOOAT01
CLONE: 724157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyt
STREET: 3174 Por
CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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US-08-933-750C-19
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  115 LEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG---- 167
                                         63 LOASROILQEEGPTAFWKGHVPAQILSIGYGAVQFLSF-----EMLTELVHRGSVYDA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 YEALPAGATVTTHM -- VAGAVAGILEHCVMYPIDCVKTRMQSLQ -----PDPPAARYRNV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%; Score 135.5; DB 4; Length 320; 28.8%; Pred. No. 2.7e-06; tive 26; Mismatches 46; Indels 27.
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Shah, very APPLICANT: Shah, very APPLICANT: Au-Young, Janice APPLICANT: Yue, Henry APPLICANT: Guegler, Karl J. APPLICANT: Corley, Neil C. TITLE OF INVENTION: HUMAN REGULATORY MOLECULES CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: September 23, 1997
ATORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECHMUNICATION INCORMATION:
TELECHMUNICATION INCORMATION:
TELECHMUNICATION INCORMATION:
TELECHMUNICATION INCORMATION:
TELECHMUNICATION INCORMATION:
TELEFAX: 415-845-4166
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                                                                                                                                                                                                                          Sequence 12, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lial, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 12:
                                                                                  168 ---NSH-IANGAAGCVATL 182
                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
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TOPOLOGY: linear
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Best Local Similarity
Matches 40; Conserv
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GENERAL INFORMATION:
APPLICANT: Gong, Weilong
APPLICANT: Branuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical Region
66 CLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHEGTRTLW----SGLPAT 122
                                                              123 LVMTVPATAIYFTAYDQLKAFLCGRALTSDLYAP------MVAGALARLGTVTVISPL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 ALPA-GATVTTH----MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALW 119
                                       138 ATGAGPAHALYFACYEKLKKTL-----SDVIHPGGNSHIANGAAGCVATLLHDAAMNPA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 311;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 59357831is, LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 RIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CH-0681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERRUCE/DOCKET NUMBER: CH-068
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                            Sequence 32, Application US/08775009
Patent No. 5935783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 33, Application US/08775009
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CTTY: Philadelphia
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US-08-775-009-32
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US-08-775-009-33
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138 ATGAGPAHALYFACYEKLKKTL----SDVIHPGGNSHIANGAAGCVATLLHDAAMNPA 191
                      ------RYRNVLEALWRIIRTEG---LWRPMRGLNVT 137
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APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Co-Hery
APPLICANT: Co-Hery
TITLE OF INVENTION: HUWAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOSS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/234,613
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       Sequence 19, Application US/09234613 Patent No. 6132973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANE: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/POCKET UNBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855.0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatib
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nes 45; Conservative
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; CLONE: 724157
US-09-234-613-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3174 Por
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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US-09-234-613-19
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Matches
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 447
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Matches 34; Conservative
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                                                                                                                                                                ORGANISM: HOMO SAPIENS US-09-160-119-4
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LENGTH: 674
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                                                                           APPLICANT: Gong, Weilong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 593783ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHGVLGLYRGLSSLLYGSIPKAAVRFGMFEFLSNHMRD 114
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Patent No. 631619
GENERAL INFORMATION:
APPLICANT: RILE, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BILL, ANTOINE
TILE REFERENCE: GH-30985
CURRENT APPLICATION: NUMBER: US/09/160,119A
CURRENT FILING DATE: 1990-09-24
EARLIER PILING DATE: 1997-10-23
EARLIER PILING DATE: 1997-10-23
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1998-07-05
NUMBER OF SEQ ID NOS: 4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 311 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-775-009-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
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    Patent No. 5935783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                    79 GAVAGILEHCVMYPIDCVKTRMQSLQPDPA----ARYRNVLEALWRIIRTEGLWRPMRGL 134
                                                                                                                                     79 GAVAGILEHCVMYPIDCVKTRMQSLQPDPA----ARYRNVLEALWRIIRTEGLWRPMRGL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
PCT-US94-09799-1
; Sequence 1, Application PC/TUS9409799
; Sequence 1, Application PC/TUS9409799
; GENERAL INFORMATION:
APPLICANT: Kagan, David
; TITLE OF INVENTION: Method and Composition for Weight Reduction
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Watov & Kipnes, P.C.
STREET: 186 Princeton-Hightstown Rd, PO Box 247
CITY: Princeton Junction
; STATE: New Jersey
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 LPQLLGVAPEKA-----IKLTVNDFVRDKFMHKDGSVPLAAEILAGGCAG 211
                                                                                                                                                                                                            135 NVTATGAGPAHALYFACYEKLKKTLSDVI-----HPGGN-----SHIANGAAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 NVTATGAGPAHALYFACYEKLKKTLSDVI-----HPGGN-----SHIANGAAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 674;
  Length 447;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
Query Match 11.1%; Score 115; DB 4; Best Local Similarity 30.1%; Pred. No. 0.00057; Matches 34; Conservative 18; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.1%; Score 115; DB 4; 30.1%; Pred. No. 0.00098;
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT FALING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09160119A Patent No. 6316219
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60 GPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALW 119
                                                                                                                                                      75 HMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 469;
                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
9.9%; Score 102.5; DB 2;
Best Local Similarity 30.7%; Pred. No. 0.011;
Matches 27; Conservative 14; Mismatches 44;
                                                                                   45;
                                                                                                                                                                                                                                            120 RIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKT 158
                                        10.3%; Score 106.5; DB 4 tilarity 30.3%; Pred. No. 0.0047; Conservative 17; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET; 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 VPSFLRLGAWNVMMFVTYEQLKRALMKV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 NVTATGAGPAHALYFACYEKLKKTLSDV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
AITLE OF INENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08937466
Patent No. 5846779
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          432 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 75 DENISE DI
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
                                          Query Match
Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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US-08-937-466-4
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US-09-172-528-4
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Fatent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Cassard, A.M. et al. publication OTHER INFORMATION: Genbank - Locus 37607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
AUTHORS: Cassard, A.M. et al.
TITLE: Human Uncoupling Protein Gene: Structure,
                      Diskette, 3.50 inch, 800 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.9%; Score 112.5; DB 5; Best Local Similarity 29.2%; Pred. No. 0.00063; Matches 26; Conservative 18; Mismatches 42;
                                                      COMPUTER: 150M
ODERATING SYSTEM: DOS 6.0
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09799
FILING DATE: 29-ANG-1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,179
FILING DATE: 25 May 1994
APPLICATION NUMBER: 08/114,313
FILING DATE: 30 AUGUST 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 KGLVPSFLRLGSWNVIMFVCFEQLKRELS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 RGLNVTATGAGPAHALYFACYEKLKKTLS 160
                                                                                                                                                                                                                                                                                                                        NAME: Kipnes, Allen R.
REGISTRATION NUMBER: 28,433
REFERENCE/DOCKET NUMBER: 485
TELECOMMUNICATION: TELECHONE: 609-243-0330
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 609-275-1010
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE: Brown adipose
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Linear
                                        IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mouse US-09-188-930-339
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LENGTH: 469
TYPE: PRT
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PCT-US94-09799-1
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75 HMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL 134
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/318,199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.9%; Score 102.5; DB 3; 30.7%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 27, 2002, 03:58:50 Job time: 4892 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELEPHONE: (650) 343-4341
TELEPHONE: (650) 343-4342
INFORMATION POSEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 NVTATGAGPAHALYFACYEKLKKTLSDV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273. VPSFLRLGAWNVMMFVTYEQLKRALMKV 300
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFCATION:
PRICA APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 30.7% Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-09-318-199-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.9%; Score 102.5; DB 2; Length 432; Best Local Similarity 30.7%; Pred. No. 0.011; Matches 27; Conservative 14; Mismatches 44; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94010

ZIP: 94010

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09318199;
Patent No. 6025469
GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                          ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE
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FILLIG DAFE:
FILLIG DAFE:
ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET WUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-434
TELEPAX: (650) 343-434
TELEPAX: (650) 343-434
TELEPAX: (650) 343-434
TELEPAX: (1650) 343-
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Sequence 4, Application US/09172528
Patent No. 5952469
GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-09-172-528-4
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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ij

Length 432;

44;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

August 27, 2002, 03:57:40 ; Search time 80.04 Seconds (Without alignments) 231.700 Million cell updates/sec Run on:

US-09-870-113-4 1036 1 MELEGRGAGGVAGGPAAGPG......GAAGCVATLLHDAAMNPAEG 193 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		prote	splic	defec	prote	defec	puc	ate	prote	prote	puc	nr	xoc	prote	prote	solut	solu	prote	rte	pr	ote	Q.	prote	Loc	Je	ein	prote	۵	ra
	uo	١				ice de	probable mitochond	probable phosphate	cal pr	cal pr	О	Btl protein precur	probable tricarbox	cal pr					ß	ADP, ATP carrier pr	hypothetical prote	probable carrier p	cal pr	adenylate transloc	probable membrane	uncoupling protein	cal pr	-	tricarboxvlate tra
	Description	hypothetical	probable RNA	mtRNA splice	hypothetical	mtRNA splice	bable	bable	hypothetical	hypothetical	bable	prote	bable	hypothetical	hypothetical	Ca-dependent	mitochondrial	hypothetical	rate t	ATP c	otheti	bable	hypothetical	nylate	bable	ouplin	hypothetical	probable	carbox
	Des	dyd G	pro	mtR	hyp	mtR	pro	pro	hyp	hyp	pro	Bt.1	pro	hyp	hyp	Ca-	mit	hyp	cit	ADP	hyp	pro	hyp	ade	pro	nuc	hyp	pro	tri
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ś	Ω	T2608	T39149	S5517	A86205	S13533	T00582	S6094	T20229	T45934	D84798	JQ1459	T37992	T43493	D84613	T47703	T01729	B96830	G0178	S31935	T0936	S5449	696770	T05350	869050	T05577	T32897	S5711	A4659
	DB	5	7	7	7	7	7	7	7	7	7	~	7	7	7	7	7	7	~	7	7	Н	7	~	7	7	7	7	2
	Length DB	312	303	314	781	304	331	307	310	358	348	436	291	351	313	332	352	296	311	301	330	905	367	392	310	313	650	322	311
æ	γď	32.7	24.3	24.3	21.7	21.6	21.5	16.2	14.5	13.8	13.7	13.0	12.8	12.6	12.5	12.4	12.4	12.0	12.0	12.0	12.0	12.0	11.9	11.8	11.7	11.7		11.6	11.6
	Score	338.5	252	251.5	224.5	223.5	223	168	150	143	142	134.5	132.5	131	129	128.5	128	124.5	124.5	124	124	124	123	122	121.5	121.5	121	120.5	120
	Result No.		7	٣	4	ഹ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28

probable mitochond mitochond	mitochondrial carr	hypothetical prote	hypothetical prote	hypothetical prote	2-oxoglutarate car	2-oxoglutarate/mal	hypothetical prote	protein K11H3.3 [i	phosphate transpor	citrate transport	uncoupling protein	probable mitochond	amino acid transpo	hypothetical prote
T51393	T29640	T23170	T16533	S54524	A56650	A36305	T24162	н88567	T01169	S44554	G01858	T50393	T47240	T51158
010	4 79	7	7	7	7	7	7	7	7	7	7	7	7	7
353	330	296	702	368	314	314	374	312	366	299	307	335	363	381
11.4	11.4	11.2	11.1	11.1	11.1	11.1	11.1	11.0	11.0	10.9	10.9	10.8	10.8	10.8
n, n	118	116	115.5	115	114.5	114.5	114.5	114	114	113	112.5	112	112	112
118.5	3		٠.											

ALIGNMENTS

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hypothetical protein W02B12.9 - Caenorhabditis elegans
C;Species: Caecasion: T26089
R;Swinburne, J.; Ainscough, R.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z20149
A;Accession: T26089
A;Status: precliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-312 <AILL>
A;Residues: 1-312 <AILL>
A;Cross-references: EMBL:Z66521; PIDN:CAA91399.1; GSPDB:GN00020; CESP:W02B12.9
A;Experimental source: clone W02B12
C;Genetics:
A;Genetics:

A;Map position: 2 A;Introns: 18/3; 251/3; 286/3 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

., Gaps Query Match 32.7%; Score 338.5; DB 2; Length 312; Best Local Similarity 48.0%; Pred. No. 8.8e-21; Matches 73; Conservative 23; Mismatches 37; Indels 19;

42 GGGEAGACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQ 101 q ö

102 SLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD 161 δ

qq

162 VIHPGGNSH-IANGAAGCVATLLHDAAMNPAE 192 ö

107 g

probable RNA splicing proteinmitochondial carrier protein - fission yeast (Schizosacc C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C; Accession: T39149
R; Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
A; Reference number: 221748
A; Accession: T39149
A; Access

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165 PGG--NSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 ANGAAGCVATLLHDAAMNP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.3%
Best Local Similarity 41.0%
Matches 57; Conservative
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Best Local Similarity
Matches 57; Conserv
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A; Residues: 1-781 <STO>
                                                                                        A;Gene: SGD:MRS3
A;Cross-references:
                                                                                                                                                  A; Map position: 10L
A; Genome: nuclear
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A; Residues: 1-86, S', 88-102, L', 104-127, Y', 129-141, M', 143-187, 'R', 189-314 <SCH>
A; Residues: 1-86, S', 88-102, L', 104-127, Y', 129-141, M', 143-187, 'R', 189-314 <SCH>
A; Cross-references: EMBL: X06239; NID: 93990; PIDN: CAA29582.1; PID: 93991
R; Wiesenberger, G.; Link, T.A.; von Ahsen, U.; Waldherr, M.; Schweyen, R.J.
J; Mol. Blol. 217, 23-37, 1991
J; Mill: MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new memt
A; Reference number: S13532; MUID: 91108815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Wolecule type: DNA
A; Residues: 1-314 cKAT>
A; Residues: 1-314 cKAT>
A; Residues: 1-314 cKAT>
A; Cross-references: EMBL: X87371; NID:9854542; PID:9854563
B; Schmidt, C.; Soellner, T.; Schweyen, R.J.
Mol. Gen. Genet. 210, 145-152, 1987
A; Titler: Nuclear suppression of a mitochondrial RNA splice defect: nucleotide sequence A; Reference number: S01267; MUID:88121698
A; Accession: S01267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-314 <KAW>
A;Cross-references: EMBL:Z49408; NID:g1008337; PID:g1008338; MIPS:YJL133w
R;Katsoulou, C.; Tazennia, M.; Tavernarakis, N.; Alexandraki, D.
Yeast 12, 787-797, 1996
A;Title: Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mtrnA splice defect-suppressing mitochondrial carrier MRS3 - yeast (Saccharomyces cerror)
N;Alternate names: protein J0675; protein VJL133w
C;Species: Saccharomyces cerevisiae
C;Date: 08-Unl-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000
C;Accession: S55179; S01267; S20228; S56915; S71664
R;Katsoulou, C.; Tzernia, M.; Alexandraki, D.
Submitted to the EMBL Data Library, May 1995
A;Description: The complete sequence of a 40.7 kb segment located on the left arm of yeast hypothetical proteins.
A;Cross-references: EMBL:299168; PIDN:CABL6300.1; GSPDB:GN00066; SPDB:SPAC8C9.12c
A;Experimental source: strain 972h-; cosmid c8C9
                                                                                                                                                                                                                                                                                                 ij
                                                                                                                A;Map position: 1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                       62 DYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 IRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 SSTEGVYSLWRGISSVIMGAGPSHAIYFSVLEFFKSK----INASPDRPLASALAGACAI 124
                                                                                                                                                                                                                                                                                                                                                                                         9 DYEGLPIGSPMYAHLLAGAFSGILEHSVMYPVDAIKTRMQMLNGVSRSVSGNIVNSVIKI 68
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A; Residues: 19-314 «MIE>
A; Cross-references: EMBL:X56445; NID:93992; PIDN:CAA39830.1; PID:93994
A; Katsoulou, C.; Tzermia, M.; Alexandraki, D.
submitted to the Protein Sequence Database, September 1995
A; Reference number: S56912
A; Accession: S56915
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A; Status: nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
                                                                                                                                                                                                                                          Length 303
                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                       24.3%; Score 252; DB 2;
40.3%; Pred. No. 1.3e-13;
tive 25; Mismatches 48;
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                                                                                                                                                                                                                                       Query Match
24.3%
Best Local Similarity 40.3%
Matches 52; Conservative
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A; Accession: S55179
                                                                                        SPDB:SPAC8C9.12c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 LLHDAAMNP 190
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A; Residues: 1-314 <KAF>
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                                                               Genetics:
                                                                                           A; Gene:
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hypothetical protein [imported] - Arabidopsis thaliana
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86205
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, A;Authors: Hutter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: A86205
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: probably involved in splicing of all intron for COB gene; essential fo
A;Cross-references: EMBL:X87371; NID:9854542; PIDN:CAA60822.1; PID:9854563
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Superfamily: ADP,ATP carrier membrane; mitochondrion; pre-mRNA splicing S;30.119,Domain: ADP,ATP carrier protein repeat homology <ACPI>F;127-211/Domain: ADP,ATP carrier protein repeat homology <ACPZ>F;216-311/Domain: ADP,ATP carrier protein repeat homology <ACPZ>F;216-311/Domain: ADP,ATP carrier protein repeat homology <ACPZ>
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PVRQDPDSGPDYEALPAGATVTTHWVAGAVAGILEHCVMYPIDCVKTRWQSLQPDPAARY 111
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Pred. No. 1.4e-13;
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probable phosphate transport protein, mitochondrial - yeast (Saccharomyces cerevisiae NyAlternate names: protein 05064; protein 708222w; protein 70850-12 (Species: Saccharomyces cerevisiae C; Species: Saccharomyces cerevisiae C; Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000 C; Accession: 850049; 857115; B37984; 871724 R;Galisson, F.; Dujon, B. submitted to the EMBL Data Library, October 1995 A; Deference number: S60938 A; Reference number: S60938 A; Reference number: S60938
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A; Residues: 1-307 <GAL>
A; Residues: 1-307 <GAL>
A; Cross-references: EMBL: X92441; NID: 91050762; PID: 91050774
B; Boyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Michaux, G.; Thierry, A.; Dujon submitted to the Protein Sequence Database, July 1996
A; Reference number: S67104
A; Accession: S67115
R;Lin, X.; Kaul. S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
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J. Biol. Chem. 265, 19736-19741, 1990
A;Title: Mitochondrial phosphate transport. N-ethylmaleimide insensitivity correlates
A;Reference number: A37984; MUID:91060585
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                                                                                                                        A;Map position: 2
A;Introns: 253/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: mitochondrion
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X;Residues: 1-307 <BOY2-
A;Cross-references: EMBL:275130; NID:91420513; PID:91420514; MIPS:YOR222w
A;Experimental source: strain S288C
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39.9%; Pred. No. 3.5e-11;
tive 22; Mismatches 51.
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A; Residues: 30, x', 32, I', 34-39 <GUE>
R; Galisson, F.; Dujon, B.
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A; Title: Sequence and ar
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A; Residues: 1-307 <GAW>
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Best Local
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                                                                                                                                                                                                              mERNA splice defect-suppressing mitochondrial carrier MRS4 - yeast (Saccharomyces cerevi
N;Alternate names: protein YKR052c
C;Spectes: Saccharomyces cerevisiae
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jul-2000
C;Accession: S13533; S38126
R;Wiesenberger, G.; Link, T.A.; von Ahsen, U.; Waldherr, M.; Schweyen, R.J.
A;Title: MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new memthaltoners s13533; MUID:91108815
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N.Alternate names: hypothetical protein T27E13.10
S.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C.Accession: T00582; C84705
S.R.Ounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, May 1998
A.Description: Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence.
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A;Residues: 1-304 <715.
A;Crosa-references: EMBL:228277; NID:9486506; PID:9486507; MIPS:YKR052c
A;Experimental source: strain S288C
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A; Residues: 11-304 <2MO.
A; Residues: 11-304 <2MO.
A; Cross-references: EMBL:X56444; NID:93995; PIDN:CAA39828.1; PID:93996
R; Vissers, S.; Urrestarazu, L.A.; Jauniaux, J.C.
submitted to the Protein Sequence Database, March 1994
A; Reference number: $38118
A; Accession: $38126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T00582
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-331 CROU>
A; Residues: 1-331 CROU>
A; Residues: BMBL: AC004165; NID: 93150396; PID: 93150404
A; Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: SGD:MRS4
A;Cross-references: SGD:S0001760; MIPS:YKR052c
   - AGDQNNSVAHAMSGVFATISSDAVFTPMD 152
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Best Local Similarity
Matches 50; Conservat
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IAADALMNP 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 11R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Genome: nuclear
                                   124
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H.W.; Lemcke, K.; Mayer, K.F

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A;Gene: At2g37890
A;Map position: 2
C;Superfamily: ADP,ATP car
C;Keywords: mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 TFPLD 286
                                                                                                                                                                                                  A; Map position: 3
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DA 266
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                                                       A;Note: YOR222w
(Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
(S;Reywords: duplication; mitochondrion; transmembrane protein
F;9-107/Domain: ADP,ATP carrier protein repeat homology (ACP1>
F;115-201/Domain: ADP,ATP carrier protein repeat homology (ACP2>
F;208-300/Domain: ADP,ATP carrier protein repeat homology (ACP3>
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A;Gene: CESP:C54G10.4
A;Map position: 5
A;Introns: 14/1: 63/1; 155/2; 256/2; 299/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted to the EMBL Data Library, June 1996
A;Reference number: 219240
A;Reference number: 219240
A;Accession: 170229
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocale type: DNA
A;Residues: 1-310 <WILL.
A;Cross-references: EMBL: 275532; PIDN:CAA99811.1; GSPDB:GN00023; CESP:C54G10.4
A;Experimental source: clone C54G10
A;Cross-references: EMBL:X92441; NID:g1050762; PIDN:CAA63185.1; PID:g1050774 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C54G10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F5K20.240 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000 C;Accetsion; T45934
                                                                                                                                                                                                                                                                                                                                                                                                      --- RYRNVLEALWRIIRTEGLW 128
                                                                                                                                                                                                                                                                                                                                                                             129 RPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 GGEAGACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVHGGTCRQ--MEDPDS------ITSHFVGGCAAGMAQSVIAAPTERIKLLLQ- 124
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                                                                                                                                                                                                                    Length 307;
                                                                                                                                                                                                                                                         54; Indels
                                                                                                                                                                                                                16.2%; Score 168; DB 2;
33.9%; Pred. No. 1.2e-06;
ilve 20; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.5%; Score 150; DB 2; 28.9%; Pred. No. 3.6e-05; Live 23; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TLSDVIHPGGNSHIANGAAGCVATLLH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGETSTLS----SGQLLFAGGTAGMLSWLFN 211
                                                                                                                                                                                                                                                                                                77 VAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA-
                                                                                                                                                                                                Query Match
Best Local Similarity 33.9%
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Best Local Similarity
Matches 44; Conserv
                                      position: 15R
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R; Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 NPAE 192
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probable mitochondrial carrier protein [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
R;Accession: D84798
M; Koo, H; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.E.; Umayam, L.; Tallon, alvere 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: D84798
A;Accession: D84798
A;Residues: 1-348 <STO>
A;Cross-references: GB:AE002093; NID:94895195; PIDN:AAD32782.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                       A; Introns: 98/3; 157/3; 207/3; 234/3; 258/2; 281/1
A;Note: F5K20.240
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 AGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 IGLYKGLGATLLGVGPSLAISFAAYETF-KTFWLSHRPNDSNAVVSLGCGSLSGIVSSTA 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 WRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAA
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R;Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, submitted to the Protein Sequence Database, January 2000 A;Reference number: Z23017
                                                                                           A;Accession: T45934
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <MON>
A;Cross-references: EMBL:AL132960
C;Genetics: Cultivar Columbia; BAC clone I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.8%; Score 143; DB 2; Best Local Similarity 28.8%; Pred. No. 0.00016; Matches 36; Conservative 23; Mismatches 56.
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RiLin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
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A;Reference number: A84420; MUID:20083487
A;Accession: D84613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Homo sapiens (man)
C.Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 CLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHEGTRTLW---SGLPAT 122
                                                                                                                                                                                     84 ILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGP 143
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                                                                -----LPAG---ATVTTHMVAGAVAG 83
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                                                                                                                       163 YRGLAATVA-----RQAANSGVRFTAYNSIKQSLQSRLPPDEKLSTVTTFLV-GSVAG
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K; Poustka, A; Klein, M; Mewes, H.W.; Gassenhuber, J.; Wiemann,
submitted to the Protein Sequence Database, December 1999
A; Reference number: Z22516
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A;Cross-references: EMBL:AL133584
A;Experimental source: adult testis; clone DKFZp434C119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 PAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.6%; Score 131; DB 2; Best Local Similarity 24.9%; Pred. No. 0.0015; Matches 45; Conservative 19; Mismatches 51,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein DKFZp434C119.1 - human
                                                             38 GRGAGGGEAGACRPPVRQDPDSGPDYEA----
                                                                                                                                                                                                                                                                                                                144 AHALYFACYEKLKKTL 159
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273 SGGIVFTVYEKVMEIL 288
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A; Residues: 1-313 <STO>
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                                                                                                                    C; Species: Zea mays (maize)
C; Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Sep-1999
C; Accession: J01459
R; Sullivan, T.D.; Strelow, L.I.; Illingworth, C.A.; Phillips, R.L.; Nelson Jr., O.E.
Plant Cell 3, 1337-1348, 1991
A; Title: Analysis of maize brittle-1 alleles and a defective suppressor-mutator-induced
A; Reference number: J01459; MUID: 93005685
A; Accession: J01459
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A;Experimental source: strain 972h-; cosmid c19G12
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 PSELYRGLTPSLIGVVPYAACNFYAYETLKRLYRRATGRRPGAD------VGPVATLLI 332
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                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-436 <SUL>
A; Cross-references: GB:M79333; NID:g168425; PIDN:AAA33438.1; PID:g168426
C; Comment: This protein acts as an adenylate translocator in amyloplasts.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 206/3; 260/3
C;Superfamily: Bt1 protein; ADP,ATP carrier protein repeat homology C;Superfamily: Bt1 protein; ADP,ATP carrier protein c;Superfamily: chloroplast; duplication; transembrane protein C;Reywords: chloroplast; deptide (amyloplast) #status predicted <TNP>F;1-75/Domain: transit peptide (amyloplast) #status predicted <ANAT>F;131-217/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;226-312/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;229-247/Domain: transmembrane #status predicted <TM1>F;323-413/Domain: transmembrane #status predicted <TM2>F;327-347/Domain: transmembrane #status predicted <TM2>
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                                                                                              Btl protein precursor
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Matches 42;
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A; Gene: At2g22500

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Ca-dependent solute carrier-like protein - Arabidopsis thaliana
N;Alternate names: protein Fill6, 50
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Sep-2000
C;Accession: T47703
E;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F. submitted to the Protein Sequence Database, March 2000
A;Reference number: 224473
A;Accession: T47703
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A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-332 <BEND:ALI61667
A:Experimental source: cultivar Columbia; BAC clone F1116
C;Genetics:
A:Map position: 3
A:Introns: 63/3; 122/3; 172/3; 206/3; 230/2; 253/1
A:Note: F1116.50
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
A;Map position: 2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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                                                                                                                                                                                                                                                130 PMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMN 189
                                                                                                                                                                                                                                                                                                                      118 LWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD - VIHPGGNSHI - ANG 174
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                                                                                                   Ouery Match 12.5%; Score 129; DB 2; Length 313, Best Local Similarity 29.7%; Pred. No. 0.002; Matches 41; Conservative 31; Mismatches 52; Indels
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GenCore version 4.5
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OM protein - protein search, using sw model

August 27, 2002, 04:16:45; Search time 37.5 Seconds (without alignments) 199.277 Million cell updates/sec Run on:

US-09-870-113-4 1036 1 MELEGRGAGGVAGGPAAGPG......GAAGCVATLLHDAAMNPAEG 193 Perfect score: Title:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P10566 saccharomyc		Q99297 saccharomyc	Q9hc21 homo sapien	zea n	Q9bqt8 homo sapien	homo	bos t	homo	homo	Q03028 saccharomyc	P33303 saccharomyc	P32089 rattus norv	Q9h2d1 homo sapien	Q27238 anopheles g		_		Q9y619 homo sapien		Q9ujs0 homo sapien	bos t		_	Q9h1k4 homo sapien	٠.	Q9qxx4 mus musculu	043772 homo sapien	P25874 homo sapien	P97700 rattus norv	_		Ogwyds musculu
SUMMARIES	ID	MRS3_YEAST	MRS4_YEAST	ODC2_YEAST	DNC_HUMAN	BT1_MAIZE	ODC_HUMAN	CG69_HUMAN	TXTP_BOVIN	TXTP_HUMAN	ORT2_HUMAN	ODC1_YEAST	SFC1_YEAST	TXTP_RAT	MFT_HUMAN	ADT_ANOGA	CMC1_DROME	M2OM_MOUSE	CMC1_CAEEL	ORT1_HUMAN	YM39_YEAST	CMC2_HUMAN	M2OM_BOVIN	M2OM_HUMAN	TXTP_CAEEL	SA18_HUMAN	TXTP_YEAST	CMC2_MOUSE	MCAT_HUMAN	UCP1_HUMAN	M2OM_RAT	AR13_NEUCR	CMC1_HUMAN	ORT1_MOUSE
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	Score	251.5	223.5	168	135.5	134.5	134	127	125	124.5	122	121.5	120.5	120		118.5	116.5	٠	115.5	115	115	115	114.5	114.5	114	114	113	113	112.5	112.5	112.5	112	112	111
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PROTEIN.

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Q10248 schizosacch P32332 saccharomyc Q9db41 mus musculu P40556 saccharomyc P39953 saccharomyc P56499 rattus nory Q12375 saccharomyc Q13375 saccharomyc Q3308 homo sapien Q97649 sus scrofa P32007 bos taurus P3641 saccharomyc
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YDIK_SCHPO PMT_YEAST SA18_MOUSE YIA6_YEAST ADT2_HUMAN UCP3_HT ORTI_YEAST PM3_HUMAN UCP3_HIG ADT3_BOVIN
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ALIGNMENTS

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Query Match
Best Local Similarity 38.88
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wiesenberger G., Link T.A., von Absen U., Waldherr M., Schweyen R.J.; "MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new members of the mitochondrial carrier family."; J. Mol. Biol. 217:23-37(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 PVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MR64 SUPPRESSES A MITOCHONDRIAL SPLICE DEFECT IN THE
FIRST INTRON OF THE COB GENE. IT MAY ACT AS A CARRIER, EXERTING
ITS SUPPRESSOR ACTIVITY VIA MODULATION OF SOLUTE CONCENTRATIONS
THE MITOCHONDRION (POSSIBLY OF CATIONS). NOT ESSENTIAL.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 314;
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                                                                                                                                                                                                                                                                                                                                                                                                               861145CE6E4EF321 CRC64;
                                                                                                                                                                                                                                                                  II (APPROXIMATE).
III (APPROXIMATE)
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                                                                                                                                                                                                                                                   I (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 251.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.3%; Score 251.5; DB 1 ilarity 41.0%; Pred. No. 1.4e-13; Conservative 18; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ou-nov-1991 (Rel. 20, Created)
15-DEC-1998 (Rel. 20, Last sequence update)
Mitochondrial RNA splicing protein MSR4.
MRS4 OR YRR052C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 AA.
                                                                                                                                                                                                                                                                                                     POTENTIAL. POTENTIAL.
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              EMBL; X56445; CAA39829.1; -.
EMBL; X56445; CAA39830.1; ALT_INIT.
EMBL; X06239; CAA29582.1; ALT_SEQ.
EMBL; X87371; CAA60822.1; -.
EMBL; X49408; CAA89428.1; -.
PIR; S01267; S01267.
PIR; S20228; S20228.
                                                                                                                                                          IPR001993; Mitoch_carrier
                                                                                                                                                                                                                                                 BLOCK
BLOCK
BLOCK
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                                                                                                                                                                         Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91108815; PubMed-1703236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 ANGAAGCVATLLHDAAMNP 190
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                                                                                                                                                                                                                                                                                                                                                                                                             34501
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                                                                                                                                                                                                                                                                                                                                      149
204
238
                                                                                                                                         S0003669; MRS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           314 AA;
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                                                                                                                                                                                                                                mRNA processing.
REPEAT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-M130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRS4_YEAST
P23500;
                                                                                                                                                             InterPro;
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REPEAT
TRANSMEM
TRANSMEM
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MRS4_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inner membrane.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. STRONG,
TO YEAST MRS3; BOTH PROTEINS MAY BE ISOFORMS OF THE SAME CARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 IRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galisson F., Dujon B.;
"Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV of the yeast Saccharomyces cerevisiae.";
Yeast 12:877-885(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2002 (Rel. 41, Last annotation update);
Mitochondrial 2-oxodicarboxylate carrier 2.
ODC2 OR YOR222W OR YOR50-12.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5ABBF9858B547EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOCK II (APPROXIMATE).
BLOCK III (APPROXIMATE).
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.6%; Score 223.5; DB 1
38.8%; Pred. No. 2.5e-11;
iive 24; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 AA.
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                                                                                                                                                                                                                                                                                                                                                                   EMBL, X56444; CAA39828.1; -.
EMBL, 228277; CAA82130.1; -.
PIR, S13533; S13533.
SGD; S0001760; MRS4.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PROSITE; PS002155; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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STRAIN=S288C / FY1679;
MEDLINE=96437977; PubMed=8840505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33307 MW;
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                  two isoforms of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 VAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA-----RYRNVLEALWRIIRTEGLW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 RPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitochondrial transporter for 2-oxoadipate and 2-oxoglutarate.";
J. Biol. Chem. 276:1916-1922(2001).
--- FUNCTION: Transports C5-C7 oxodicarboxylates across the inner membranes of mitochondria. Can transport 2-oxoadipate, 2-oxoglutarate, adipate, glutarate, 2-oxopimelate, oxaloacetate, citrate and malate. The main physiological role is probably to supply 2-oxoadipate and 2-oxoglutarate from the mitochondrial matrix to the cytosol where they are used in the biosynthesis of lysine and glutamate, respectively, and in lysine catabolism.
--- SUBCELLUIAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palmieri L., Agrimi G., Runswick M.J., Fearnley I.M., Palmieri F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrffini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; Lravello Carr; 3.
Pram; PROD155; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
Prochondrion; Inner membrane; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
8
                                                                                                                                                                                                 -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.2%; Score 168; DB 1; Length 307; 33.9%; Pred. No. 7.8e-07; Live 20; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4089082A64DBA97C CRC64;
                                                "Identification in Saccharomyces cerevisiae of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
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EMBL; X92441; CAA63185.1; -.
SGD; S0005748; ODC.
InterPro; IPR002067; Mit.carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34007 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215
280
307 AA;
                                                                                                                                                                                        inner membrane
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01-MAR-2002
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Q9HC21;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the uptake of deoxynucleotides into the FUNCTION: Responsible for the uptake of deoxynucleotides into the matrix of the mitochonding. Transports all four deoxy NDPs, and, less efficiently, the corresponding dNTPs. Does not transport dNMPs, NMPs, deoxynucleosides, nucleosides, purines, or pyrimidines. Supply deoxynucleotides to the mitochondrial matrix for conversion to triphosphates and incorporation into mitochondrial DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- DISBASE: Likely to be medically important by providing the means of uptake into mitochondria of nucleoside analogs, leading to the mitochondrial impairment that underlies the toxic side effects of such drugs in the treatment of viral illnesses, including AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 YEALPAGATVTTHM--VAGAVAGILEHCVMYPIDCVKTRMQSLQ-----PDPAARYRNV 114
                                                                                                  Dolce V., Fiermonte G., Runswick M.J., Palmieri F., Walker J.E.; "The human mitochondrial deoxynucleotide carrier and its role in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          placenta. Highest levels in colon, kidney, lung, testis, spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 320;
SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and in cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                    "MUP 1, a mitochondrial uncoupling protein."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57CE0F01D538B1BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.1%; Score 135.5; DB 1; 28.8%; Pred. No. 0.00035; iive 26; Mismatches 46;
                                                                                                                                                           toxicity of nucleoside antivirals.";
Proc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                     Renard S., Mondesert G., Besnard F.; "MUP 1, a mitochondrial uncoupling pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pram; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001993; Mitoch_carrier
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ301616; CAC37793.1; -. AF182404; AAG16903.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ251857; CAC27560.1; -.
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BC005120; AAH05120.1;
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193
313
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320 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                               PubMed=11226231;
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Best_Local Similarity 31.7
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                              SLC25A21 OR ODC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion;
                              185 DAA 187
                                                                                     333 GSA 335
                                                                                                                                                                                                                                   ODC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                              280 PSELYRGLTPSLIGVVPYAACNFYAYETLKRLYRRATGRRPGAD------VGPVATLLI 332
                                                         LEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG---- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAGATVTTHWVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEG 126
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YDPKPDGRNNTKFQVAVAGSVSGLVTRALISPFDV1K1RFQ-LQHERLSRSDPSAKYHGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of maize brittle-1 alleles and a defective Suppressor-mutator-induced mutable allele."; Plant Cell 3:137-1348[1991).
-I- FUNCTION: COULD PLAY A ROLE IN AMYLOPLAST MEMBRANE TRANSPORT.
-I- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
-I- TISSUE SPECIFICITY: ENDOSPERM OF DEVELOPING KERNELS.
-I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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PRINTS; PR00926; MITOCH_CARRIER; 1.
PROSITE; PS000215; MITOCH_CARRIER; 1.
Transit peptide; Chloroplast; Amyloplast; Transmembrane.
TRANSIT 1 75 CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-93005685; PubMed-1668652;
Sullivan T.D., Strelow L.I., Illingworth C.A., Phillips
Nelson O.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9600C05F603E9DAE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Brittle-1 protein, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                                  436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                          ---NSH-IANGAAGCVATL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M79333; AAA33438.1; -.
                                                                                                                                                                                                                                116 REFSVHFVCGGLAACMATL 134
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JQ1459; JQ1459.
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Best Local Similarity
Tabes 42; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays (Maize)
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P29518;
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                                                      115
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                                                                                                                                                                       168
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                                                                                                                                                                                                                                                                                                                                                    BT1_MAIZE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
MEDLINE=11269385; PubMed=11083877;
Fiermonte G., Dolce V., Palmieri L., Ventura M., Runswick M.J.,
Palmieri F., Walker J.E.;
Identification of the human mitochondrial oxodicarboxylate carrier:
Identification of the human mitochondrial characterization,
tissue distribution and chromosomal location.";
J. Biol. Chem. 276:8225-8330(2001).
I- FUNCTION: Transports C5-C7 oxodicarboxylates across the inner
membranes of mitochondria. Can transport 2-oxodipate, 2-
oxoglutarate, adipate, glutarate, and to a lesser extent,
pimelate, 2-oxopimelate, 2-aminoadipate, oxaloacetate, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 MVAGAVAGILEHCVMYPIDCVKTR--MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 INVTATGAGPAHALYFACYEKLKKTLSDV-IHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane; Repeat; Transmembrane; Transport.
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.9%; Score 134; DB 1; Length 299; 31.7%; Pred. No. 0.00043; ive 26; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69A259400328AE19 CRC64;
                                                                       01-WAR-2002 (Rel. 41, Created)
01-WAR-2002 (Rel. 41, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
299 AA
                                                                                                                                                                                           Mitochondrial 2-oxodicarboxylate carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
PRT;
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Best Local Similarity 23.8%
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
142
181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::| |
175 TVTVISPLE 183
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EMBL;
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Suyano S.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional prediction of the coding sequences of 79 new genes deduced by analysis of cDNA clones from human fetal liver."
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1/CGI-69L (shown here) and 2; are produced by alternative splicing.
-!- TISSUE SPECIFICITY: Expressed in many tissues. Abundant in testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan G., Adams S.H.;
"Overexpression of the human 2-oxoglutarate carrier lowers mitochondrial membrane potential in HEK-293 cells: contrast with the Unique cold-induced mitochondrial carrier CGI-69.";
Biochem. J. 353:369-375(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=11139402;
Yu X.X., Lewin D.A., Zhong A., Brush J., Schow P.W., Sherwood S.W.,
                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Baueraachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner D., ambutt R., Korn B., Klein M., Poustka A.; acatalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome. Res. 11:422-435(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Ch' ang L.-Y., Liu C.-S., Lin W.-C.;
"Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
Genome Res. 10:703-713(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and kidney.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                          CG69_HUMAN STANDARD; PRT; 359 AA. 09B2J4; 09UF66; 09X379; 09PB2; 001F67. 001F6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inner membrane
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Liver;
                                                   RESULT 7
CG69_HUMAN
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                                                                                                                                        DDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 PAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAA----------- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RYRNVLEALWRIIRTEG---LWR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 PMRGLNVTATGAGPAHALYFACYEKLKKTL-----SDVIHPGGNSHIANGAAGCVATLL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
11-NOV-1997 (Rel. 40, Last nonctation update)
11-Cort-2001 (Rel. 40, Last annotation update)
11-Cort-boxylate transport protein, mitochondrial precursor (Citrate transport protein) (CTP) (Tricarboxylate carrier protein).
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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: ::| :| || || 66 SSLQSTGKCLLYCNGVLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHEGTRTLW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
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LPSSLQSTG -> W (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.3%; Score 127; DB 1; Length 359; 23.8%; Pred. No. 0.0019; ive 19; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> R (IN REF. 6).
952AA3DB5F5F9BD1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
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EMBL; BC009330; AAH09330.1; -.
EMBL; AF119864; AAF69618.1; -.
InterPro; IPR001993; Mitcoh_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                  EMBL, AF317711; AAG60687.1; -. EMBL, AF151027; AAD34064.1; -. EMBL, AL133584; CAB63728.1; -. EMBL, AK026060; BAB15341.1; -.
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SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ξ,
                                                                                  Biochim. Biophys. Acta 1284:9-12(1996).
-i- FUNCTION: INVOLVED IN CITRATE-H+/MALATE EXCHANGE. IMPORTANT FOR THE BIOENERGETICS OF HEPATIC CELLS AS IT PROVIDES A CARBON SOURCE FOR FATTY ACID AND STEROL BIOSYNTHESES, AND NAD+ FOR THE
                    Iacobazzi V., de Palma A., Palmieri F.;
"Cloning and sequencing of the bovine cDNA encoding the mitochondrial
tricarboxylate carrier protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AGATVTTH----MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYTP_HUMAN STANDARD; PRT; 311 AA.
P53007; Q9BSK6;
10.CGT-1996 (Rel. 34, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
11-MAR-2002 (Rel. 41, Last annotation update)
11-MAR-2003 (Citrate transport protein) (CTP) (Tricarboxylate carrier protein).
                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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Heisterkamp N., Mulder M.P., Langeveld A., ten Hoeve J., Wang 2.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRICARBOXYLATE TRANSPORT PROTEIN
                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.1%; Score 125; DB 1; Length 311; Best Local Similarity 30.6%; Pred. No. 0.0024; Matches 30; Conservative 22; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITOCHONDRION (BY SIMILARITY)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                              DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 TEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD 161
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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PROSITE; PS00215; MITOCH_CARRIER; 1.
  MEDLINE-97019278; PubMed-8865808;
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311
46
105
                                                                                                                                                                                GLYCOLYTIC PATHWAY
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311 AA;
                                                                                                                                                                                                                            inner membrane
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                                                                                                                                                                                                            Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: INVOLYBD IN CITEATE-H+/MALATE EXCHANGE. IMPORTANT FOR THE BIOENTRGETICS OF HERALIC CELLS AS IT PROVIDES A CARBON SOURCE FOR FATTY ACID AND STEROL BIOSYNTHESES, AND NAD+ FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 ALPA-GATVTH----MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALW 119
Roe B., Groffen J.; "Localization of the human mitochondrial citrate transporter protein gene to chromosome 22q11 in the DiGeorge syndrome critical region."; Genomics 29:451-456(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITOCHONDRION (BY SIMILARITY).
TRICARBOXYLATE TRANSPORT PROTEIN.
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F1341629924953D6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 RIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD 161
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                                                                                                                                                                                                                                                                                                                                                                                              -! - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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31.4%; Pred. No. 0.00.
+ive 22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 1.
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01-WAR-2002 (Rel. 41, Last seq
01-MAR-2002 (Rel. 41, Last anno
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EMBL; BC004980; AAH04980.1; -.
EMBL; BC008061; AAH08061.1; -.
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34012 MW;
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202
241
297
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                                                                                                                                                                                                                                                                                                                                                                      inner membrane
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nes 32; Conserv
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                                                                                                                                                            TISSUE=Kidney;
Strausberg R.;
                                                                                                                                    SEQUENCE FROM
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Q9BXI2;
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Walker J.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                      Genome Res. 11:389-404(2001).

-I- FUNCTION: Ornithine transport across inner mitochondrial membrane, from the cytoplasm to the matrix (By similarity).

-I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).

-I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

-I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97313271; PubMed=9169875;
Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,
Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,
Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,
Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                              SEQUENCE FROM N.A. MEDIINE-21154914; PubMed-11230163; MEDIINE-21154914; PubMed-11230163; Wu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz J., Bickson M., Noonan J.P., Zhang M.Q., Myers R.M., Maniatis T.; "Comparative DNA sequence analysis of mouse and human protocadherin
Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial 2-oxodicarboxylate carrier 1.
Mobil 0R YPL134C OR LPIIIC.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Rungi; Ascomycota; Saccharomycotina; Saccharomycetaies; Saccharomycetaes;
                                                                                                                                                                                                                                                                                                                                                                                    membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.8%; Score 122; DB 1; Length 301; 33.3%; Pred. No. 0.0041; Live 16; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 VTATGAGPAHALYFACYEKLKKTL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 ATMIRAIPANGALFVAYEYSRKMM 294
                                                                                                                                                                                                                                                                                                                                 EMBL; AF332005; AAK26320.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32580 MW;
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Best Local Similarity 33.34
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         88
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257
            Eutheria;
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210
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301 AA;
 Metazoa;
                      NCBI_TaxID=9606;
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Q03028;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Midentification in Saccharomyces cerevisiae of two isoforms of a novel mitochondrial transporter for 2-oxoadipate and 2-oxoglutarate."; U. Biol. Chem. 276:1916-1922(2001).

- FUNCTION: Transports C5-70 oxodicarboxylates across the inner membranes of mitochondria. Can transport 2-oxoadipate, 2-oxoadipate, citrate and malate. The main physiological role is probably to supply 2-oxoadipate and 2-oxoglutarate from the mitochondrial matrix to the cytosol where they are used in the biosynthesis of lysine and glutamate, respectively, and in lysine catabolism.
Delius H., DiPaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U., Johnston M., Kalman S., Klache K., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F., Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A., Purnelle D., Schafer M., Scharfe M., Schrems B., Schramm S., Schreens B., Schramm S., Schreens B., Schramm S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
                                                                                                                                                                                                                                                                                                                                                                                    Hani J.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."; Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 AGAVAGILEHCVMYPIDCVKTRMQ---SLQPDPAA-----RYRNVLEALWRIIRTEG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 LWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHI------ANGAAGCV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palmieri L., Agrimi G., Runswick M.J., Fearnley I.M., Palmieri F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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219
281
310 AA;
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11013234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S00006055;
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precursor (Citrate

311 AA.

PRT;

STANDARD;

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J. Biol. Chem. 268:13682-13690(1993).
-!- FUNCTION: INVOLVED IN CITRATE H+/AMLATE EXCHANGE. IMPORTANT FOR THE BIOENERGETICS OF HEATIC CELLS AS IT PROVIDES A CARBON SOURCE FOR FATIT ACID AND STEROL BIOSYNTHESES, AND NAD+ FOR THE
                                                                                                                                                                                                                                                                                                           Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primary structure, and comparison with other mitochondrial transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaplan R.S., Mayor J.A., Wood D.O.;
"The mitochondrial tricarboxylate transport protein. cDNA cloning,
                                                                                                                                                      01-OCT-1993 (Rel. 27, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
11-Ticarboxylate transport protein, mitochondrial precursor transport protein) (TTP) (Tricarboxylate carrier protein) SLC25A1 OR SLC20A3.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver; MEDLINE-93293897; PubMed-8514800;
                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLYCOLYTIC PATHWAY
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins.
                             13
                             RESULT
                                                                                    ALD DE COURT OF THE COURT OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLUIAR LOCATION: Integral membrane protein, Mitochondrial, -1- INDUCTION: BY ETHANOL OR ACETATE AS SOLE CARBON SOURCES, REPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product as a succinate-fumarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VREHLENLGIFKKNDTPKPKPLK -> RKGAFQKIWVYSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- FUNCTION: Transports cytoplasmic succinate, derived from isocitrate by the action of isocitrate lyase in the cytosol, into the mitochondrial matrix in exchange for fumarate.
                                                                          Succinate/fumarate mitochondrial transporter (Regulator of acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHÄRACTERIZATION.
MEDLINE-98055465; PubMed-9395087;
Palmieri L., Lasorsa F.M., De Palma A., Palmieri F., Runswick M.J.,
                                                                                                                                                                                                                                                                                                   MEDLINE-94203187; PubMed-7908717; Medicio R.; Rernandez M., Fernandez E., Rodicio R.; RACR1, a gene encoding a protein related to mitochondrial carriers, is essential for acetyl-CoA synthetase activity in Saccharomyces cerevisiae.";
                                                                                                                                                                                 Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ramezan1 Rad M., Kirchrath L., Hollenberg C.P.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of the yeast ACR1 gene product as a succ
transporter essential for growth on ethanol or acetate.'
FEBS Lett. 417:114-118(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTHQSQSH (IN REF. 1).
EC29718A0F5011A7 CRC64;
                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.6%; Score ... 32.5%; Pred. No. 0.0058
                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00153; mito_carr; 3. PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Gen. Genet. 242:727-735(1994).
                                                                                                                         SFC1 OR ACR1 OR YJŘÓ95W OR J1921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Transport; Repeat
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(Rel. 28, (Rel. 32,
                                             01-MAR-2002 (Rel. 41,
                                                                                                    synthetase activity)
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Best Local Similarity
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$43280; $43280
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                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AGATVTTH----MVAGAVAGILEHCVMYPIDCVKTRMOSLOPDPAARYRNVLEALWRIIR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                              Pfan; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 1.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRION.
TRICARBOXYLATE TRANSPORT PROTEIN.
                                                 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C7B5B8D82311F6D6 CRC64;
                                   DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 120; DB 1;
; Pred. No. 0.0061;
23; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 TEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHGVLGLYRGLSSLLYGSIPKAAVRFGMFEFLSNHMRD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                                                                                                                                                                 PR001993; Mitoch_carrier.
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311
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311 AA;
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TRANSIT
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86
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4.

Gaps

Indels 13;

45;

Conservative

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DB 1; Length 322;

Score 120.5; DB Pred. No. 0.0058;

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Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
  01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August 27, 2002, 04:16:46 Job time: 1238 sec
                                                                                                                                                                                                                                                                                                    MEDLINE=94348635; PubMed=8069414;
01-NOV-1997 (Rel. 35, 01-NOV-1997 (Rel. 35, 01-NOV-1997 (Rel. 35,
                                                                                               translocator) (ANT)
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                      NCBI_TaxID=7165;
                                                                                                                                                                                      Anopheles
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SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ′,
                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE=20538421; PubMed=10978331;
Titus S.A., Moran R.G.;
"Retrovirally mediated complementation of the glyB phenotype. Cloning of a human gene encoding the carrier for entry of folates into mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 LWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLK -- KTLSDVIHPGGNSHIANGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 AGATVITH-----MVAGAVAGILEHCVMYPIDCVKTRMQ-----SLQPDPAARYRNVLEA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mitochondria.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro: InterPro: InterPro: InterPro: InterPro: InterPro: Pro0153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
Mitochondrion; Inner membrane; Pepeat; Transmembrane; Transport.
Prochondrion; Inner membrane; PoreNITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 275:36811-36817(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- TISSUE SPECIFICITY: Ubiquitous.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. 60EBCOD61951EB6E CRC64:
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Pred. No. 0.0068;
                                                                                                                                      01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
11-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial folate transporter/carrier.
                                                                                           315 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF283645; AAG37834.1; -.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                           PRT;
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315 AA; 35388 MW;
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27.5%;
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                                                                                           STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                        MFT_HUMAN
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Q27238;
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SEQUENCE
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ID ADT_AI
AC Q27231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                     Insect Mol. Biol. 3:35-40(1994).
-!- FUNCTION: CATALIZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
-!- SUBDNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Transmembrane; Transport. (POTENTIAL).
Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.; "A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                             -!- DOMAIN: COMPOSED OF THREE HOWOLOGOUS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 VTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
4CC9E17C9F8DA08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.4%; Score 118.5; DB 1; 29.2%; Pred. No. 0.0078; wiematches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carri 3.
PRNRYS; PR00936; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane;
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136
197
233
293
6
32863 MW;
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Matches 31; Conservative
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                                                                                                                                                                                                        inner membrane
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TRANSMEM 14
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August 27, 2002, 04:19:20 ; Search time 130.92 Seconds (without alignments) 255.026 Million cell updates/sec
                                                                                                                                                                                                             US-09-870-113-4
1036
1 MELEGRGAGGVAGGPAAGPG......GAAGCVATLLHDAAMNPAEG 193
                                                                                                                                                                                                                                                                                                                                                                                                               562222
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                  562222 seqs, 172994929 residues
                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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SPTREMBL_19:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_lnvertebrate:*
6: sp_anman:*
7: sp_mc:*
8: sp_organelle:*
9: sp_phage:* sp_vertebrate:*
sp_unclassified:* sp_rvirus:* sp_bacteriap:* sp_archeap:* sp_plant: *
sp_rodent: *
sp_virus: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		10000	Describrion	Q96a46 homo sapien	Q920g8 mus musculu	Q9nyz2 homo sapien		Q91zy0 mus musculu	Q23125 caenorhabdi	Q9vay3 drosophila	Q9nhy6 drosophila	Q94638 onchocerca	Q94634 onchocerca	014281 schizosacch	Q91mj6 arabidopsis	064731 arabidopsis	O82049 ribes nigru	Q9d547 mus musculu	Q9ax03 oryza sativ
SUMMARIES		£		Q96A46	Q920G8	Q9NYZ2	096981	Q912Y0	Q23125	Q9VAY3	9 XHN6O	094638	094634	014281	95m160	064731	082049	Q9D547	Q9AX03
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		or COS	30016	1030	516.5	515.5	444.5	444.5	338.5	295	291	267.5	265.5	252	224.5	223	211	158.5	155.5
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150 14.5 310 5 018844 144.5 13.9 320 11 0921P8 143.5 13.9 459 5 09VKZ5 143.13.8 358 10 09K33 142 13.7 413 10 09K33 142 13.7 413 10 09K89 139 5 32 WFF9 130 13.4 10 09KF9 130 5 13.2 304 4 09WKZ 136 5 13.2 304 4 09WKZ 136 5 13.2 304 4 09WKZ 136 13.1 32 34 11 09CKZ 136 13.1 320 4 09KZZ 136 13.1 320 4 09KZZ 131 12.9 299 4 09KZZ 131 12.9 301 10 09AZZ 131 12.6 310 4 09WZZ 131 12.6 310 10 09ZZZG 131 12.6 311 1 09ZZZG	Q18844 caenorhabdi Q921p8 mus musculu Q9vtz5 drosophila Q9vi05 drosophila Q9wi05 drosophila	arab roso ratt omo omo	Q9Cw38 mus musculu Q9ma27 arabidopsis Q9hc21 homo sapien Q9cyj1 mus musculu Q9pt18 homo sapien Q9ar19 hordeum vul	013844 schizosacch 099vbn7 drosophila 09vgm3 drosophila 09nvn5 homo sapien 0962290 mus musculu 097379 homo sapien 092379 tomo sapien 092379 tomo sapien 093779 tomo sapien 094375 arabidopsis 094312 drosophila
144.50 144.5 144.5 142.5 142.5 142.5 136.5 136.5 137.5 137.5 137.5 137.5 131.5	310 5 0 320 11 5 0 3 399 5 0 4449 5 0 8 358 10	.7 348 10 .4 298 11 .3 321 4 0 .2 304 4 0	22 334 11 319 10 10 345 11 325 11 53 55 11 55 55 55 55 55 55 55 55 55 55 55	291 3 0 2 2 3 1 3 0 2 3 1 3 1 4 1 4 1 4 1 4 1 4 1 4 1 4 1 4 1
	ιΩ · · · · · ·	142 142 139 137.5 136.5	136.5 136.5 134.5 134.5 133.5	132.5 131.5 131.5 131 131 131 131 130 128

ALIGNMENTS

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Query Match
Best Local Si
Matches 106;
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  IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
                        121 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Li Q.-2., Ruan Q.-G., Eckenrode S., Shi J.-D., Cruz P., Wang C.-Y., She J.-X.,
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A new gene which is highly expressed in NOD mice spleen."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF288621; AAL23859.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Song H., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
"A novel gene expressed in human hypothalamus.";
Submitted (JAN.2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF223466; AAF64141.1;
InterPro. IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MELRRGGVGNQAAG------RRMDGDCRDG---GCGSKDAGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 AA; 37510 MW; BB35B1F70C56A3FE CRC64;
                                                                                                                                                                                                                                                                                              (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 516.5; DB 11;
Pred. No. 2e-37;
                                                                                                                                                                                                                                                       338 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRIAL SOLUTE CARRIER-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.9%; Sco
54.7%; Pre
tive 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 105; Conservative
                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                      181 TLLHDAAMNPAE 192
                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-HYPOTHALAMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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01-DEC-2001
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                                                                                                                                                                                                                                                     Q920G8
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121
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PDYEALPAGATVTTHWVAGAVAGILEHCVMYPIDCVKTRMOSLOPDPAARYRNVLEALWR 120
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                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., She J.;
protein
                                                                                                                                                                                                                                                 1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Li Q., Eckenrode S., Ruan Q., Wang C., Shi J., McIndoe R.A., She J "Molecular cloning of a novel mictochondria solute carrier protein ("MCP) gene from mouse and human and its down-regulation in mouse spleen during the maturation of the immune system.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                   IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 EDYENLPISASVSTHMTAGAMAGILEHSVMYPVDSVKTRMOSLSPDPKAQYTSIYGALKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANG 174
                                                                                                                                        Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MITOCHONDRIA SOLUTE CARRIER PROTEIN (HYPOTHETICAL 16.8 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AY012628; AAK38154.1; -.
EMBL; BC015013; AAH15013.1; -.
Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 347 AA; 37828 MW; 700DE61B230E001E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8ACB98A483C8E6EF CRC64;
                                                                                                                                     49.8%; Score 515.5; DB 4; ilarity 55.2%; Pred. No. 2.5e-37; Conservative 20; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.9%; Score 444.5; DB 4 52.9%; Pred. No. 1.6e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-UTERUS, AND LEIOMYOSARCOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 155 AA; 16832 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||||| |||||
154 TLLHDAVMNPAE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                               Local Similarity
nes 106; Conserv
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Matches 92; Conserv
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us-09-870-113-4.rspt

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Query Match
Best Local Similarity 48.09
Matches 73; Conservative
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                                                                                                                                                                                                                                                                                                                                     Q9VAY3;
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09VAY3
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L1 0., Eckenrode S., Wang C., Ruan Q., Shi J., McIndoe R.A., She J.;
L1 0., Eckenrode S., Wang C., Ruan Q., Shi J., McIndoe R.A., She J.;
A novel mouse mitochondrial carrier protein gene is up-regulated from young to adult NOD mice.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF361699; AAL27990.1;
SEQUENCE 182 AA; 19838 MW; 18E2C5E801228693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PDYEALPAGATVTTHWVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MELRRGGVGNQAAG------RRMDGDCRDG---GCGSKDAGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANG 174
                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 42.9%; Score 444.5; DB 11; Length 182; Best Local Similarity 52.3%; Pred, No. 2e-31; Matches 91; Conservative 18; Mismatches 38; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swinburne J., Ainscough R.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
Science 282:2012-2018(1998).
EMBL; 266521; CAA11399.1; -
Interpro; IPRO01993; Mitoch_carrier.
Pfam; PF00153; Mitoch_carris; 9.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 312 AA; 34093 MW; D65FC4DD2936F76A CRC64;
                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MITOCHONDRIAL CARRIER-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                   NCBI_TaxID=10090;
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W02B12.9.
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                                                                                  Q912Y0;
01-DEC-2001
01-DEC-2001
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Q23125;
                                                                  Q912Y0
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
A pandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
Ballew R.M., Cawley S., Dehlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Deller H., Caddeu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Deller C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Balle C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Balle C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,
RA Burtis R.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser R.,
Allouston K.A., Gong F., Gorrell J.H., Gu Z., Genna P., Harris M.,
RA Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Hacklum K.A.,
Alli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alli M., Matlush F., Karpen G.H., Ke Z., Kennison J.A., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Murphy D., Lai Z.,
Liang Y., Lin X.,
Rallander K., Moy M., Murphy B., Murphy L., Murphy C., Morits J., Moshrefi A.,
Melson D.R., Nelson K.A., Nixon K., Murphy C., Morits J., Moshrefi A.,
Ra Balazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ra Balazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ra Balazzolo M., Pittman G.S., Langson M., Strong R., Shen H.,
Spier E., Spradling A.C., Staplecon M., Strong R., Shen H.,
Spier E., Spradling A.C., Staplecon M., Strong R., Shan B.,
Wang Z.-Y., Wassarman D.A., Welly, Venter E., Wang A.H., Wang S., Yan W., Woodage T., Wood., Wang S., Lang G., Mang S., Lang 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                42 GGGEAGACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQ 101
                                                                                                                                                                                      102 SLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD 161
                                                  Gaps
                                                                                                                     19;
  Length 312;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
32.7%; Score 338.5; DB 5;
48.0%; Pred. No. 7e-22;
iive 23; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                           379 AA
                                                                                                                                                                                                                                                                               162 VIHPGGNSH-IANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
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61; Conservative
Best Local Similarity
Matches 61; Conserv
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01-JUN-2001
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Q94634
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                                            62
                                                                                                                                                                                                                         RESULT
094638
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                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                         62 DYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                               122 IRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    61
 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE CO B SECOND SECOND SECOND STAIN—I, CO BW STEPIN P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Minoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                         5 DYESLPT-TSVGVNWTAGAIAGVLEHVVWYPLDSVKTRWQSL--SPPTKNWNIVSTLRTW
                                                                                                                                                                                                                                                                                                                                                                 ;
9
                                                                                                                                      INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AE003763; AAL25764.1; -.
FURBS; FBG00039561; C4963.
INTERPO; IPR001993; Mitoch_carrier.
InterPro; IPR001993; Mitoch_carrier.
PR00153; mito_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CANTON-S:

A Schmid K.J., Tautz D.;
Schmid K.J., Tautz D.;
Schmid K.J., Tautz D.;

"A screen for rapidly evolving genes from Drosophila.";
"A screen for rapidly evolving genes from Drosophila.";
"Explain AF217402; A8773387.1;

R FlyBase; FB90003951; GG9963.

R InterPro; IPR001993; Mitcoh.carrier.

R Pfam; PF00153; mitc.carrier.

R PRINTS; PR00926; MITCOARRIER.

R PRINTS: PR00926; MITCOARRIER.
                                                                                                                                                                                                                                                                                                                                   Length 379;
                                                                                                                                                                                                                                                                                                                                                                41; Indels
                                                                                                                                                                                                                                       Pfam; PF00153; micclarrier.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH CARRIER; 2.
Inner membrane; Mitochondrion; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41844 MW; 4C9AA524B97F8C6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0c7-2000 (TrEMBLrel. 15, Created)
01-0c7-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TEMBLrel. 17, Last annotation update)
HYPOTHETICAL 41.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                   28.5%; Score 295; DB 5;
47.3%; Pred. No. 5.6e-18;
tive 22; Mismatches 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l protein.
380 AA; 4
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:||| :| |:
119 LIHDAISSPTD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 LLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
SEQUENCE 38
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Length 380;

DB 5;

28.1%; Score 291;

Query Match

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5
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                                                                                                                                                                                            62 ITREGLIRPIRGASAVVLGAGPTHSLYFAAYEMTKELTAKFTSVRNLNYVISGA---VAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 CRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 ARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYEALPAGATVTTHWVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRI 121
                                                                                                                                                                     122 IRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 CRWPV------HILLAGSVAGLAEHCLMFPFDSVKTRLQSLCPCPE 50
                                                                                                      Onchocerca gibsoni.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
NCBL_TaxID=6284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Onchocerca volvulus.
Bukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
Onchocercidae, Onchocerca.
NCBI_TaxID=6282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.8%; Score 267.5; DB 5; Length 303; 37.5%; Pred. No. 1.1e-15; Live 26; Mismatches 41; Indels 23
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitochondrial solute carriers.";
Biochim. Biophys. Acta 1282:179-181(1996).
Biochim. Biophys. Acta 1282:179-181(1996).
InterPro; IPR001993; Mitoch_carrier.
Priam; PF00153; mito_carrier.
Prostre; PS00215; MITOCH_CARRIER; UNKNOWN 2.
SEQUENCE 303 AA; 33861 WW; 224BFA547E5D617C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               094638;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 02, Last sequence update) (TrEMBLrel. 17, Last annotation update)
               Pred. No. 1.3e-17;
; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TrEMBLrel. 02, Created)
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109 NSVSYAISGALATVIHDAVMNPAE 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 SHIANGAAGCVATLLHDAAMNPAE 192
46.68; Fit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 37.5
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                              182 LLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                         |:||| :| | :
119 LIHDAISSPTD 129
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SEQUENCE FROM N.A.
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Liu S.X., Chan A., Yu G., Etgu P., Lee J.M., Lenz C., Pham P., Sakano H., Torlumi M., Chung M., Goldsmith A., Liu A., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A., Hansen M., Johnson-Hopson C., Khan S., Kin C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;

The sequence of BAC Floki from Arabidopsis thaliana chromosome 1.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

InterPro; IPR001933; Mitc.Arrier.
                122 IRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVAT 181
                                   69 SSTEGVYSLWRGISSYIMGAGPSHAIYFSVLEFFKSK----INASPDRPLASALAGACAI 124
                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 PVRQDPD----SGPDY--EALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 PDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00153; mito_carr; 4.
PRINTS; PR00926; MITOCH_CARRIER:
PROSITE; PS00215; MITOCH_CARRIER: UNKNOWN_2.
SEQUENCE 781 AA: 87081 MW; 9FB579B9BD746D1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE MITOCHONDRIAL CARRIER PROTEIN.
                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.7%; Score 224.5; DB 1
38.0%; Pred. No. 1.9e-11;
tive 23; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                            781 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 -AGDQNNSVAHAMSGVFATISSDAVFTPMD 152
                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                        (TrEMBLrel. 15, (TrEMBLrel. 15, 1) (TremBLrel. 19, 1)
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                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
F10K1.26 PROTEIN.
                                                                              182 LLHDAAMNP 190
                                                                                                           125 TISDAFMTP 133
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                          01-0CT-2000
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064731;
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                                                                                                                                                                                            OPLMJ60
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064731
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                                                                                                                                                            RESULT
Q9LMJ6
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             Catmull J., Miller D.J.; "CDNAs from Onchocerca sp. encoding members of the MRS3/MRS4 class of
                                                                                                                                                                                                                                                        49 CRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPA 108
                                                                                                                                                                                                                                                                                                                     109 ARYRNVLEALWRIIRTEGLWRPWRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGN 168
                                                                                                                                                                                                                                                                                                                                         51 TSCPTAMHSLMSMVKREGLLRSLKGVNAVVLGTIPAHAFYYTVYENSKAYLLN--NPRVS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 DYEALPAGATVTTHMVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRI 121
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                      ------HLLAGSVAGLAEHCLMFPFDSVKTRLQSLCPCPE 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 DYEGLPIGSPMYAHLLAGAFSGILEHSVMYPVDAIKTRMQMLNGVSRSVSGNIVNSVIKI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.,
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!-SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                          Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; 299168; CAB16300.1; -.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 303;
                                                                                                                                                                                                                          Indels
                                           mitochondrial solute carriers.";
Biochim. Biophys. Acta 1282:179-181(1996).
EMBL; U45997; AMBH9036.1;
InterPro; IPR001993; Mitoch_carrier.
Pfam, PF00153; mito_carris.
PROSTIE: PS00215; MITOCH_CARRIER; UNKNOWN 2.
SEQUENCE 301 AA; 34176 MW; COBABDB19FB8EA79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
69975CDE18107AB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                        ; Score 265.5; DB 5;
; Pred. No. 1.7e-15;
26; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 252; DB 3;
Pred. No. 2.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Hypothetical protein; Mitochondrion; Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequenc
01-JUN-2001 (TrEMBLrel. 17, Last annotat
PUTATIVE MITOCHONDRIAL CARRIER C8C9-12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                       169 SHIANGAAGCVATLLHDAAMNPAE 192
MEDLINE=96326580; PubMed=8703971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                                       25.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228
32652 1
                                                                                                                                                                                                                        54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                      12 CRWPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
164
208
303 AA;
                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Best Local S:
Matches 52,
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SEQUENCE
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Best Local S
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Hayashizaki Y.;
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Q9D547;
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S
                                                             STRAIN-CV. COLUMBIA;
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodnan H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 PVRQDPDSGPDYEALPAGATVTT----HMVAGAVAGILEHCVMYPIDCVKTRMQSLQPD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 PIPQPPDFHP---AIIVPAQNTTLKFWQLMVAGSIAGSVEHMAMFPVDTVKTHMQALRSC 72
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that
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-!-SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotá; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Saxifragales; Grossulariaceae; Ribes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC004165; AAC16956.1; -.
InterPro; IPR01993; Mitoch_carrier.
Pfam; PF00153; Mitocarr; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 331 AA; 35961 MW; AODE93084BEC8BC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MITOCHONDRIAL CARRIER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.5%; Score 223; DB 10; 39.9%; Pred. No. 9.7e-12; tive 22; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ДK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 G--NSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |: |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |
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STRAIN-CV. BEN ALDER; TISSUE-FRUIT;
Woodhead M.R.;
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Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                              Nature 402:761-768(1999).
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                                              SEQUENCE FROM N.A.
NCBI_TaxID=3702;
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STRAIN-C57BL/63; TISSUE=TESTIS;

KRAIN-C57BL/64; TISSUE=TESTIS;

KRANI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Fukunishi Y., Konoo S., Yamanaka I.,

Raito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsudo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Ruonstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ruonstein M.J., Bult C., Fletcher C., Fujita M., Manbaerts P.,

Ruschine D., Rang B., Ringwald M., Rodiguez I., Sakamoto N.,

Rosaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Ruschinal M., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Ruschinal M., Washida K., Rasegawa Y., Kawaji H., Rohtsuki S.,

Ruschinal M., Vandor K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 MVAGAVAGILEHCVMYPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLN 135
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:||:|| :|| || |||:| :||:|:|:
| MIAGSIAGSIEHMAMYPVDTLKTRIQAI-GSCSAQSAGLRQALGSILKVEGPAGLYRGIG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AMGLGAGPAHAVYFSVYEMCKETFS---HGDPSNSGAHAVSGVFATVASDAVITPMD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 VTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MELEGRGAGGVAGGPAAGPGRSPGESALLDGWLQRGVGRGAGGGEAGACRPPVRQDPDSG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
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-i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. EMBL; AJ007580; CAA07568.1; -.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mitoch_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 289 AA; 30383 MW; 5666EAB03DCC507C CRC64;
                                                                                                                                                                                                                                                                                                                       Length 289;
                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                       20.4%; Score 211; DB 10; 38.5%; Pred. No. 9.4e-11;
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Pred. No. 1.7e-06;
9; Mismatches 22
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EMBL; AK015790; BAB29978.1; -.
MGD; MGI:1922377; 4930513014Rik.
                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 17, C. (TrEMBLrel. 17, L. (TrEMBLrel. 17, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1930513014RIK PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
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Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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Search completed: August 27, 2002, 04:19:22 Job time: 1289 sec

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us-09-870-113-8.rag

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Human uncoupling p
Human transport pr
Human polypeptide
Human polypeptide
Human ORFX ORF2744
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Human mitochondria
Human mitochondria
Novel human secret
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ORFX ORF398
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| SIDS1/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDS1/gcddata/geneseqy-embl/AA1981.DAT:*
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| SIDS1/gcddata/geneseqy-embl/AA1990.DAT:*
| SIDS1/gcddata/geneseqy-embl/AA2001.DAT:*
| SIDS1/gcddata/geneseqy-embl/AA2001.DAT:*
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1406
1 MOSLQPDPAARYRNVLEALW.......VYEFFKYLITKRQEEWRAGK
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4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                            747574 segs, 111073796 residues
GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Listing first 45 summaries
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AAM41505
AAM39719
AAB42980
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                                                                                      OM protein - protein search, using sw model
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AAB40634
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Human protein SEO Human mitochondria Human mitochondria Human polypeptide, Human polypeptide, Human secreted pro Human protein SEO Drosophila melanog O volvulus mitoch Human secreted pro Gene #25 human sec Blackcurrant RIB7 Arabidopsis thalia	Human ORFX ORF2732 Human ORFX ORF2728 Novel human diagno Human ORFX ORF2730 Drosophila melanog Drosophila melanog Human Uncoupling p Human ORFX ORF2547 Arabidopsis thalia Drosophila melanog Human ORFX ORF3136 Human Polypeptide	ve; antiarthritic; ; vasotropic; cterial; opthalmological; ical; vulnerary; thrombolytic; sease; thrombosis; arthritis;
199 22 AAM80023 187 22 AAM89822 187 22 AAB89822 187 22 AAB98222 187 22 AAB98222 188 21 AAB33112 29 22 AAB33112 29 22 AAB3112 215 22 AAB49666 194 21 AAB32111 181 22 AAB49666 194 21 AAB32111 181 22 AAB49666 194 21 AAB32019 299 18 AAM77054 270 21 AAG22079 270 21 AAG22079 270 21 AAG3093 270 21 AAG43093 270 21 AAG43093	22 22 22 22 22 23 22 23 23 24 25 25 25 27 27 27 27 27 27 27 27 27 27 27 27 27	Protein; 289 AA. t entry) rotein #6. protein; immunosuppressi iproliferative; cardiant neuroprotective, antiba nephrotropic; gynaecolog er; wound; infectious di 0-US09534. S-0128701. S-0142821. S-0149448.
25.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.	34.3.5 34.3.5 30.9 26.1.5 26.1.5 243.5 243.5 17. 242.5 17. 242.5 17. 242.5 17. 242.5 17. 242.5 17. 242.5 17. 242.5 17. 242.5 17. 242.5 17. 242.5 17.	RESULT AAB50383 XX AAB50383; AC AAB50383; AC AAB50383; AX XX MUMAN uncoupling proceeding antimentic; a
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Soppet DR;

Rosen CA,

Ni J, Komatsoulis G,

Ruben SM,

(HUMA-) HUMAN GENOME SCI INC

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26-DEC-2000; 2000WO-US34263.
       (INCY-) INCYTE GENOMICS INC
                         Yue H,
                          Yang J, Yue H,
IR, Azimzai Y,
                                                       WPI; 2001-041424/05
                                                                 N-PSDB; AAF27733
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                                     Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukaemia.
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                                                                                 The present sequence is a human uncoupling protein. The nucleotide sequences encoding the uncoupling proteins may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human: transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder; immune disorder; cancer.
                                                                                                                                                                                                                                                                                                                                                                        SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNE 120
                                                                                                                                                                                                                                                                                                      9
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                           Uncoupling proteins and nucleic acid sequences encoding them, usefu for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders
                                                                                                                                                                                                                                                      1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
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                                                                                                                                                                                                              100.0%; Score 1406; DB 21; Length 289; 100.0%; Pred. No. 3.1e-153; Live 0; Mismatches 0; Indels 0;
                                                                    Claim 11; Page 323-324; 343pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Human transport protein TPPT-33.
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99US-0148177.
99US-0149357.
99US-0162287.
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                                                                                                                                                                                                                                    Conservative
 2000-656322/63
                                                                                                                                                                                                                         Best Local Similarity
Matches 265; Conserv
                                                                                                                                                                                     289 AA;
           N-PSDB; AAC90457
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10-AUG-1999;
18-AUG-1999;
28-OCT-1999;
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                                                                                                                                                                                                                  Query Match
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                                                                                                                                          Isolated polypeptide with a human transport protein sequence is useful for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular systems \cdot
Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 289;
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  Hillman JL, Tang YT, Bandman
Lu DAM, Au-Young J, Patterson
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Local Similarity 100.0%; Pred. No. 3.1e-153;
Nes 265; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                               Claim 2; Page 133-134; 165pp; English.
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                           Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 318
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(first entry)

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzhaner's; Parkinson's disease; Huntington's disease, haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                     Human polypeptide SEQ ID NO 2864.
                                            22-OCT-2001
                                                                                                                                                                                                                                     Leukaemia.
  AAM39719;
  NAME OF THE PROOF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, famunosoppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinhibhin activity, chemotactic/chemokinetic activity, haemotactic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                    Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GAGAFYRSYTTQLTMNVPFQAIHFWTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPST
                                                                                                                                                                                                                                                    Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 318;
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Yang Y,
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                                                                                                                                                                                                                                                  hen R, Ma Y, (
Xu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 6436; 10078pp; English.
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Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
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2000US-0662191.
2000US-0693036.
                                       2000US-0552317.
2000US-0598042.
                   2000US-0488725
                                                                                 2000US-0620312
                                                                                                                                          19-OCT-2000; 2000US-0693036
29-NOV-2000; 2000US-0727344
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                                                                                                                                                                                                                                                                                                                                   2001-442253/47.
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                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAI60661
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                                                       09-JUL-2000;
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                                                                                                                      14-SEP-2000;
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Best Local Si
Matches 265,
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                                                                                                                                                                                                                                                                      Wang
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AAM39719 standard; Protein; 268 AA

RESULT AAM39719

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic attainst sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and thrombolytic activity, arthritis and inflammation, leukaemias and constants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1377; DB 22;
Pred. No. 6.2e-150;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 2864; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                           Asundi V, Che
Wehrman T, Xu
Goodrich R,
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                                                                                                                                                                                                                             2000US-0598042.
2000US-0620312.
2000US-0653450.
                                                                                                                                                                                   2000US-0488725,
2000US-0552317.
                                                                                                                                   26-DEC-2000; 2000WO-US34263
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2000US-0693036
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Matches 260; Conservative
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N-PSDB; AAI58875.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, F
Wang Z, V
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 AA;
                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                         WO200153312-A1.
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Homo sapiens.
                                                                                                                                                                                                                             09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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25-APR-2000;
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                                                                                         26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QA,
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AAM00938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antitizal; antibacterial; antifugal; antirhemmatic; antithyroid; antianaemic; gene therapy; cancer; prolliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                             Human; open reading frame; ORPX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsrtinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
181 TPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPST 240
                                   GAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAAT 180
                                                ×
                                                                                             frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                       Human ORFX ORF2744 polypeptide sequence SEQ ID NO:5488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 4662-4663; 5507pp; English.
                                                                                                                                 265
                                                                                                                                            AAB42980 standard; Protein; 272 AA.
                                                                                                                               241 AIAWSVYEFFKYLITKRQEEWRAGK
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99US-0127728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0127607
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                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-602362/57.
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05-APR-1999;
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                    antinflammatory; antibacterial; antivital; antifuggal; antirheumatic; antinflammatory; antibacterial; antivital; antifuggal; antirheumatic; the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORRY-associated disorder. The nucleic acids can be used to express ORRX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, proliferative disorders, neurodegenerative disorders, osteoarthritis, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anemnia, burns, wounds, bone and cartilage damage, nocturnal heemoglobinuria, antinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Length 272;
antidiabetic; hypotensive; dermatological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.1%; Score 1013.5; DB 21
69.7%; Pred. No. 4.9e-108;
ive 39; Mismatches 40;
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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Best Local Similarity 69.79
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 AA;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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AAB40634;
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                                                                                                                                                                                                         The present sequence is one of 251 novel human polypeptides encoded by a bone marrow-expressed polynucleotide. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKORMOMYNSPYHRVTDCVRAVWONE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPLDVCKTLLNTQESLALN-SHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                   Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOSLOPDPAARYRNVLEALWRITRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAAT
                                                            rord JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y
Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J;
Zhao QA, Zhou P, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 999.5; DB 22
Pred. No. 3.1e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein encoded by gene #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Mismatches
                                                                                                                                                                                      Claim 10; Page 504-505; 648pp; English.
                                                                                                                                                                                                                                                                                                                                                                    compounds as potential drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU01989 standard; Protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 TAIAWSVYEFFKYLITKROEEWRA 263
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taiswsvyeffkyfltkrqlenra 364
                                                                                                                                                                                                                                                                                                                                                                                                                             71.1%;
68.6%;
           2000US-0693036.
2000US-0250583.
14-SEP-2000; 2000US-0662191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                 WPI; 2001-488707/53
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                           366 AA;
                                                                                                                               N-PSDB; AAH90057
                      30-NOV-2000;
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Best Local Simi
Matches 181;
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The sequence represents a human secreted protein encoded by a nucleic acid of the invention. Secreted proteins and their related nucleic acids can be used in the diagnosis of or susceptibility to a pathological condition by determining the presence or absence of a mutation in a nucleic acid or the presence or amount of expression of a secreted protein. The sequences are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The antibodies to the polypeptides can also be used in alleviating symptoms associated with disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). The disorders include autoimmune diseases e.g. rheumatoid arthritis, hyperpoliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. candiac arrest, viruses and cuisal dound healing and epithelial cell proliferation, to help
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Forty one nucleic acid molecules encoding human secreted proteins, useful
in the prevention, treatment and diagnosis of cancer, immune disorders,
nervous system disorder; bacterial infection; viral infection; fungal infection; ocular disorder; wound healing; tissue regeneration; epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prevent skin ageing due to sunburn, to maintain organs before transplantation, to regenerate tissues, in chemotaxis and as a food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 ITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  additive or preservative to alter storage capabilities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 916; DB 22;
Pred. No. 4.3e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 501; 518pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.1%; Scur.
100.0%; Pre
0; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                         99US-0155807.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Komatsoulis G, Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-281684/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 174; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS03906
                                                                                                                                                                                                WO200123598-A1
                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-1999;
                                                                                                                                                                                                                                                                                                                            26-SEP-2000;
                                                                                                                                                                                                                                                            05-APR-2001
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Gaps

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Indels

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Mismatches

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Matches 172; Conservative

213

265

64

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Claim 11; Page 854; 5507pp; English.
                                                                                                                02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                     31-MAR-2000; 2000WO-US08621
                                                                      thrombosis; contraceptive.
                                                                                                                                       Shimkets RA, Leach M;
                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                               WPI; 2000-602362/57.
                                                                                                                                                   N-PSDB; AAC74843
                                                                                     WO200058473-A2
                                                                              Homo sapiens.
                                                                                                            31-MAR-1999;
   08-FEB-2001
                                                                                             05-0CT-2000
                                                                                                                                                                                                                                                                        Sequence
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94 VVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEH 153
                                                                                                                                                               human mitochondrial solute carrier (hMSC) protein isomer and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a human mitochondrial solute carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mitochondrial solute carrier (hMSC-homologue) protein SEQ:7.
                                                   154 FNPORRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAF
                                                                                                                                                                                                                                                                        214 RIVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQEEWRAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; hMSC; hMSC-homologue; mitochondrial solute carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 18 (disclosure); 22pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB98221 standard; Protein; 176 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JUN-2000; 2000CN-0116795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (first entry)
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Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li N, Xu X, Xiao H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-282781/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH22162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB98221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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AAB98221
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                                                                                                                                                                                                                                                                        antianaemic; gene therapy; cancer; proliferative disorder; hypertension; meurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyrcidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria, autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation;
                                                                                                      Human, open reading frame, ORFX, detection, cytostatic; hepatotropic, vulnerary, antipsoriatic, antiparkinsonian; nootropic, neuroprotective; anticonvulsant; ostoopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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                                                      Human ORFX ORF398 polypeptide sequence SEQ ID NO:796.
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Pred. No. 2.2e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.7%; S
100.0%;
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(first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                   Gaps
protein, designated hMSC-homologue, which is expressed in human hypophysis. Also described are methods for the preparation and detection of hMSC-homologue protein and nucleotide sequences. The present sequence represents hMSC-homologue, as given in the present
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                          Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 RTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQEEWRAGK
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                   64.7%; Score 910; DB 22;
100.0%; Pred. No. 2.2e-96;
ive 0; Mismatches 0;
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(first entry)

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18-DEC-2001
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                                                                                                                                                                                                                                                                                                                The invention relates to a novel human mitochondrial solute carrier protein, hMSC-0 (AAB60658), and cDNA encoding it (AAF59920). hMSC-0 is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-0 proteins and nucleic acids, and the detection of hMSC-0 proteins and nucleic acids in a sample. The present sequence represents hMSC-0.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                 New human mitochondrion solute carrier protein and its nucleic acid
                                                                                                            solute carrier protein; hMSC-o; hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 331;
125 rtvyqvggvtayfrgvqarviyqipstaiawsvyeffkylitkrqeewragk 176
                                                                                                                                                                                                                                                                                                                                                                                                                     36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human mitochondrial solute carrier protein hMSC-o.
                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 848.5; DB 2
; Pred. No. 6.7e-89;
34; Mismatches 36
                                                                                                                                                                                                                      (SREN-) SOUTHERN RES CENT NAT HUMAN GENE GROUP.
                                        AAB60658 standard; Protein; 331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU29748 standard; Protein; 677 AA.
                                                                                                                                                                                                                                                                                                 Claim 4; Page 20; 21pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                     60.3%;
68.4%;
                                                                                                                                                                                     17-MAR-2000; 2000CN-0114958.
                                                                                                                                                                                                     17-MAR-2000; 2000CN-0114958
                                                                           (first entry)
                                                                                                                                                                                                                                       Zhang X, Gao X, Xiao H;
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 68.4
Matches 154; Conservative
                                                                                                                   preparation; detection
                                                                                                                                                                                                                                                       2001-050544/07.
                                                                                                           mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                             331 AA
                                                                                                                                                                                                                                                                 N-PSDB; AAF59920
                                                                                                                                    Homo sapiens.
                                                                                                                                                    CN1269409-A.
                                                                                                                                                                     11-OCT-2000
                                                         AAB60658;
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU29748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
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                                 AAB60658
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                       RESULT
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. They may be used to the proteins are useful in genetic vaccination, testing and the proteins are useful in genetic vaccination, testing and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU3510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                    Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPLDVCKTLLNTQESLALN-SHITGHI 206
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Novel human secreted protein #239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0552929.
2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-2001; 2001WO-US08656
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Matches 138; Conserv
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                                                                                                                                                                                                                           Homo sapiens
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26-JAN-2001;
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Best Local S
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AAM80023 RESULT

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clones. 830 cDNA molecule encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
synthesizing full length cDNA clones and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID NO 4059; 1380pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.6%; Score 725.5; DB 22; Length
71.9%; Pred. No. 4.3e-75;
.ive 27; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashi K, Ishii S,
K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; full length cDNA; cDNA synthesis; oligo-capping.
                                                                                                                                                                                                                                                                           AAM93909 standard; Protein; 187 AA.
                                                                                                                                                                                                                                                                                                                                                                                             Human polypeptide, SEQ ID NO: 4059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishikawa T, Isogai T,
su A, Sugiyama T, Nagal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.
02-MAY-2000; 2000JP-0183765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-2000; 2000EP-0114089.
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                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                      254 ITKRQEEWRA 263
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188 ltkrglenra 197
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Best Local 8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                 gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Жa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene thy
accine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang ZW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.6%; Score 739.5; DB 22;
llarity 71.6%; Pred. No. 1.2e-76;
Conservative 27; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 409-410; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful in diagnosis and gene therapy -
                                    AAM80023 standard; Protein; 199 AA.
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Zhao QA, Wang D, Wang J, Zhi
Xue AJ, Yang Y, Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0560875.
2000US-0598075.
2000US-0620325.
                                                                                                                                                        Human protein SEQ ID NO 3669
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                                                                                                              06-NOV-2001 (first entry)
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Matches 136; Conserv
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20-JUN-2000; 2
19-JUL-2000; 2
01-SEP-2000; 2
15-SEP-2000; 2
                                                                                                                                                                                                                                                                                             Homo sapiens.
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30-NOV-2000;
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Kawai Y; T, Koga

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Gaps

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135 MNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQE 194

Sequence

Query Match Best Local 9

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Length 187;

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              140 QAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTOESLALN 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human mitochondrial solute carrier (hMSC) protein isomer and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a human mitochondrial solute carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein, designated hMSC-homologue, which is expressed in human hypophysis. Also described are methods for the preparation and detection of hMSC-homologue protein and nucleotide sequences. The present sequence represents the human mitochondrial solute carrier hMSC protein sequence which is given in comparison with the hMSC-homologue protein sequence in an example from the present
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                                                                                                                                                                                                                                                               Human mitochondrial solute carrier (hMSC) protein sequence.
                                                                                                                                                                                                                                                                                        Human; hMSC; hMSC-homologue; mitochondrial solute carrier,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 4.3e-75;
7; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
                                                                                                                                                                                     AAB98222 standard; Protein; 187 AA
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llarity 71.9%; Pr
Conservative 27;
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                                                                                                                                                                                                                                      20-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xiao H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-282781/30.
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                                                                                                                      181 lenra 185
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                                                                                                                                                                                                                                                                                                                                                                                          27-JUN-2000;
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                                                                                                                                                                                                              AAB98222;
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                                                                                                                                                             RESULT 14
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(MSC) protein represented by sequence AAB49665, which is encoded by cDNA sequence AAC92501. The protein is expressed in adrenal gland tissue. The invention includes methods for the preparation of the protein and
                                                                                                                                                                                                                                                                                                                                                                                              New human mitochondrial solute carrier protein and its coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a human mitochondrial solute carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPF 139
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                                                                                                                                                 Human mitochondrial solute carrier (MSC) amino acid sequence.
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                                                                                                                                                                        Mitochondrial solute carrier; MSC; human; adrenal gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27; Mismatches
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                                                                              AAB49665 standard; Protein; 187
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 2; 21pp; Chinese.
                                                                                                                                                                                                                                                                   2000CN-0111774
                                                                                                                                                                                                                                                                                         2000CN-0111774
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.69
Best Local Similarity 71.99
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                     Li N, Qian B, Peng Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-050472/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 AA;
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                     181 lenra 185
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259 EEWRA 263
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STRAIN: Ben Alder US-09-068-140A-10
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                                                                             August 27, 2002, 03:58:50 ; Search time 48.11 Seconds (without alignments) 134.541 Million cell updates/sec
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Sequence 15, Appl
Sequence 19, Appl
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Sequence 4, Appli
Sequence 2, Appli
Sequence 12, Appl
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1 MOSLQPDPAARYRNVLEALW......VYEFFKYLITKRQEEWRAGK 265
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Sequence 1
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTuS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-068-140A-15
US-09-234-613-19
US-09-188-930-339
US-09-188-930-339
US-09-160-119-4
US-09-160-119-4
US-09-33-750C-12
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US-09-318-199-4
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US-09-318-199-4
US-09-318-199-4
US-08-775-009-33
US-08-775-009-33
US-08-775-009-33
US-08-318-199-2
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US-09-142-565-2
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US-09-946-719A-56
US-08-937-466-6
US-09-172-546-6
US-09-118-199-6
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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Sequence 6, Appli Sequence 56, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 10, Appl Sequence 10, Appl Sequence 37, Appl Sequence 4, Appli
US-09-503-579-6 US-08-18-878B-56 US-08-608-718-878B-51 US-08-607-861A-51 US-08-607-861A-51 US-09-10-681-51 US-09-10-681-51 US-09-18-970-142 US-09-18-970-142 US-09-18-970-142 US-09-18-970-142 US-08-19-18-978-37 US-08-19-18-978-37 US-08-10-681-37 US-08-10-681-37 US-08-10-681-37 US-08-10-681-37 US-08-10-681-37 US-09-10-681-37 US-09-10-681-37 US-09-10-681-37
4-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1
256 299 299 309 309 309 303 303 303 303 303 303 3
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148 137 137 121 121 121 106 106 106 106 106 106 106 106
44444 85011484556886444444

ALIGNMENTS

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18-59-140A-10

18-59-GENELAL HOLD APPLICATION US/09068140A

PRETENT NO 6211409

GENERAL INFORMATION:

PAPPLICANT: MATY Rose Woodhead, Mark Andrew Taylor APPLICANT: MATY Rose Woodhead, Mark Andrew Taylor TITLE OF INVENTION:

PAPPLICANT: MATY ROSE WOODHEAD Brennan

TITLE OF INVENTION:

MURBER OF SEQUENCES: 15

CONFESSONDEMCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: MAY OF Prussia

STATE: PA

COMPITE: INP C COMPATION:

MEDIUM TYPE: Floppy disk

COMPITER: IEM PC COMPATION:

MEDIUM TYPE: PACHOLIN DATA:

APPLICATION NUMBER: DC-DOS/MS-DOS

SOFTWARE: PACHOLIN BATA:

APPLICATION NUMBER: US/09/068,140A

FILING DATE: NO. 6281409ember 4, 1996

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: C70237

FILING DATE: NO. 6281409ember 4, 1996

ATTORNEY/AGENT INFORMATION:

PROJESTRATION NUMBER: 33,680

ATTORNEY/AGENT INFORMATION:

TELECOMMUTCATION OF SEQUENCE THRACETERISTICS:

LENGTH: 289 amino acids

TOPOLOGY: unknown

MOLECULE TYPE: Peptide

HYPOTHETICAL: YEE

HYPOTHETICAL: YEE

MOLECULE TYPE: HOP AGEN INFORMATION:

TOPOLOGY: UNKNOWN

MOLECULE TYPE: HOP AGEN INFORMATION:

SEQUENCE THREE PROFILES INFORMATION:

MOLECULE TYPE: HOP AGEN INFORMATION:

STRAMBENDERS: UNKNOWN

MOLECULE TYPE: HOP AGEN INFORMATION:

STRAMBENDERS: UNKNOWN

MOLECULE TYPE: HOP AGEN INFORMATION:

STRAMBENDERS: UNKNOWN

MOLECULE TYPE: HOP AGEN INFORMATION:

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                                                                                                                                                                                                               9 AARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG 68
                                                                                                         11;
                                    Length 289;
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Patent No. 6281409
GENERAL INFORMATION: 
GENERAL INFORMATION: 
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APPLICATION NUMBER: US/09/068,140A
                                30.5%; Score 429.5; DB 4;
38.7%; Pred. No. 1.6e-42;
iive 38; Mismatches 108;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: No. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C7(
TELECOMMUNICATION:
TELEPHONE: 610-270-5017
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SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
HYPOTHETICAL: YĒS
ANTI-SENSE: NO
FRAGMENT TYPE: N·terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 WSVYEFFKYLITKRQE 259
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                                                                                                                                                                    11;
                                                                                                                          Length 328;
                                                                                                                                                                    Indels
                                                                                                                        30.5%; Score 429.5; DB 4;
38.7%; Pred. No. 2e-42;
ive 38; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil G.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: September 23, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY_AGENT INFORMATION:
NAME: Billings, Lucy J.
RESISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08933750C Patent No. 5932442
GENERAL INFORMATION:
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Hillman, Jennifer L.
Bandman, Olga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 WSTYEASKTFFOKLNE 320
                     Ribes nigrum
                                                                                                                          Query Match 30.5
Best Local Similarity 38.7
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 WSVYEFFKYLITKROE 259
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
; ORIGINAL SOURCE:
; ORGANISM: Ribes ni
; STRAIN: Ben Alder
US-09-068-140A-15
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CLASSIFICATION:
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APPLICANT:
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61 ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 ALTSDLYAP------MVAGALARLGTVTVISPLELMRTKLQAQHVSYRELGACVRTAV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 ONEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFN---PORRYNPSSHVLSGACAGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 AQGGWRSLWLGWGPTALRDVPFSALYWFNYELVKSWLNGLRPKDQTSVGMSFVAGGISGT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 VAAAATTPLDVCKT----LLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 VAAVLTLPFDVVKTQRQVALGAMEAVRVNPL---HVDSTWLLLRRIRAESGTKGLFAGFL 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTL--- 60
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Fatent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILICATION DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 17.9%; Score 251.5; DB 4;
Best Local Similarity 27.8%; Pred. No. 2.7e-21;
Matches 75; Conservative 43; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 219.5; DB of the conservative 47; Mismatches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 ARVIYQIPSTAIAWSVYEFFKYLITKRQEE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 PRIIKAAPSCAIMISTYEFGKSFFQRLNQD 346
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                           INFORMATION FOR SEQ ID NO: 19: SEQUEBNCE CHARACTERISTICS: LENGTH: 351 amino acids TYPE: amino acid
                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                  ; IMMEDIATE SOURCE:
; LIBRARY: SYNOOAT01
; CLONE: 724157
US-09-234-613-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
'Loca 73; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Mouse US-09-188-930-339
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                                                                                                            TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                               61 ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 AQGGWRSLWLGWGPTALRDVPFSALYWFNYELVKSWLNGLRPKDQTSVGMSFVAGGISGT 259
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTL--- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 QNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFN---PQRRYNPSSHVLSGACAGA
                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                    Length 351;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                  ; Score 251.5; DB 2;
; Pred. No. 2.7e-21;
43; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: EastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| || || || || : :: 317 PRIIKAAPSCAIMISTYEFGKSFFQRLNQD 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 ARVIYQIPSTAIAWSVYEFFKYLITKRQEE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/09234613 Patent No. 6132973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
      INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                    17.9%;
27.8%;
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                                            LENGTH: 351 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 27.8<sup>3</sup>
Matches 75; Conservative
                       SEQUENCE CHARACTERISTICS LENGTH: 351 amino acid TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yue, Henry
APPLICANT: Guegler, Ka
APPLICANT: Corley, Nei
                                                                                                     ; TOPOLOGY: linear
; IMMEDIATE SOURCE:
LIBRARY: SYNOOAT01
; CLONE: 724157
US-08-933-750C-19
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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STATE: CA
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US-09-234-613-19
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67 GGN----SHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVR----AVW 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 QNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHF-NPQRRYNPSSHVLSGACAGAVA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 AAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| : ::| || : || 370 YKNSFDCFKKVLRYEGFFGLYRGLLPQLLGVAPEKA-----IKLTVNDFVRDKFMHK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVI----HP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.1%; Score 213; DB 4; Length 674; 26.7%; Pred. No. 2.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0
                                                              TITLE OF INVENTION NOVEL COMPOUNDS
FILE REPERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: EP 97402511.6
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOUTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-933-750C-12; Sequence 12, Application US/08933750C; Patent No. 5932442; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Conservative
                      APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 IPSTAIAWSVYEFFK 251
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                                                                                                                                                                                                                                                                                                                                                                                                         CRGANISM: HOMO SAPIENS US-09-160-119-2
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Best Local Similarity
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CITY: Palo Alto
STATE: CA
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                        328 AKEGVAAFYKGYIPNMLGIIPYAGIDLAVYETLKNTW--LQRYAVNSADPGVFVLLACGT 385
                                                                                                                                                                                                                                       171 CAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: :| | | :| :| :| 195 DGSVPLAAEILAGGCAGGSQVIF----TNPLEIVKIRLQVAG----EITTGPRYSALSVV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 V----IHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNS-PYHRVTDCVRAVW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 QNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHF-NPQRRYNPSSHVLSGACAGAVA 176
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218 ASRSNNMCIVGGFTQMIREGGAKSLWRG-NGINVLK--IAPESAIKFMAYEQMKRLVGSD 274
                                                                                         275 QETLRIH---ERLVAGSLAGAIA----QSSIYPMEVLKTRMALRKTGQYSGMLDCARRIL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 GGN----SHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVR----AVW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: || || || || || 307 ASLVTPADVIKTRILQVAARAGQTTY----SGVIDCFRKILREEGPKALWKGAGARVFRS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVI-----HP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.1%; Score 213; DB 4; 26.7%; Pred. No. 1.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUGHEY, MICHEL
APPLICANT: SOUGHEY, MICHEL
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILING DATE: 1998-09-24
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1997-0-23
NUMBER OF SEQ ID NOS: 4
SSCIENARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5: SEQ ID NOS: 4
LENGTH: 447
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Sequence 4, Application US/09160119A
Patent No. 6316219
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                                                                                                                                                                                                                                                                                                                                   231 ARVIYQIPSTAIAWSVYEFFK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: HOMO SAPIENS
US-09-160-119-4
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Best Local Similarity
Matches 68; Conserv
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64 IHPGG-----NSH-IANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSP--YHRVTDCV 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 GTMYRSEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEGKKNENLQNLLC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 GSGAGVISKTLTYPLDLFKKRLQVGGFEHARAAFGQVRRY-KGLMDCAKQVLQKEGALGF 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACAGAVAAAATTPLDVCKTLLNT---QESLALNSHITGHITGMASAFRTVYQVGGVTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.1%; Score 212.5; DB 4; 23.4%; Pred. No. 9.6e-17; Live 54; Mismatches 116;
                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhang, Ning
APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
APPLICANT: Chen, Jin-Long
APPLICANT: Chen, Jin-Long
NUMBER OF SEQUENCES: 6
CORRESPONDENCES: 6
CORRESPONDENCES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                               PF-0356 US
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Sequence 4, Application US/08937466

Patent No. 5846779

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 12:
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 15.1%
Best Local Similarity 23.4%
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
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CLONE: 207452
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STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE
                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CLONE: 2
US-09-234-613-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 VHRGSVYDAREFSVHFVCGGLAACMATL----TVHPVDVLRTRFAAQGEPKVYNTLRHAV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 RAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFN-----PQRRYNPSSHVLS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 GTMYRSEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEGKKNENLQNLLC 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 212.5; DB 2; Length ; Pred. No. 9.6e-17; 54; Mismatches 116; Indels
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CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
             APPLICATION NUMBER: US/08/933,77:
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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282 FKGLSPSLLKAALSTGFMFFSYEFF 306
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Hillman, Jennifer L.
Bandman, Olga
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                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.45
Matches 62; Conservative
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LIBRARY: SPLNNOT02; CLONE: 207452
US-08-933-750C-12
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                                                                                                                           FILING DATE:
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APPLICANT:
APPLICANT:
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APPLICANT:
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US-09-234-613-12
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64 IHPGGNSHIANG---AAGCVATLLHDAAMNPAEVVKQRMQMY-----NSPYHRVTDCV 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 432;
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Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09318199; Patent No. 6025469; GENERAL INFORMATION: APPLICANT: Chang, Ming APPLICANT: Chang, Ming APPLICANT: Chen, Jin-Long TITLE OF INVENTION: UCP3 Genes NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESSE: SIENCE 75 DENISE DRIVE CITY: HILLSBORDGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 RVIYQIPS--TAIAWSVYEFFKYLITKR 257
SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/937,466
                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-(
TELECOMMUNICATION INFORMATION:
TELEFHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
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: USA
                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-172-528-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFA-----CYEKLKKTLSDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
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ADDRESSE:
ADDRESSE:
ATRET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acids
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APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09172528
Patent No. 5952469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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TITLE OF INVENTION: NO. 5935783el Genes Mapping in the Digeorge and TITLE OF INVENTION: Vellocardiofacial Syndrome Minimal Critical Region NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSE: Moodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 IHPGGNSHIANG---AAGCVATLLHDAAMNPAEVVKQRMQMY-----NSPYHRVTDCV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : : | | : : | | : : | | 1.1 | : | | 1.1 | : | | 1.1 | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 -- PKGADHSSVAIRILAGCTTGAMAVTCAQPTDVVKVRFQAMIRLGTGGERKYRGTMDAY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 RAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRY--NPSSHVLSGAC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 AGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 SVQYRGVLGTILTMVRTEGPRSPYSGL----VAGLHRQMSFASIRIGLYDSVKQFYT-- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFA-----CYEKLKKTLSDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.5e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 168.5;
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: OSNAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
ITELEPHONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 -----VPSFLRLGAWNVMMFVTYEQLKR 295
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                                                                                                                                  US/08/937,466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gong, Weilong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.0%;
24.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 amino acids
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Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-503-579-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: One Libert;
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/09/503,579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.0%; Score 168.5; DB 3; 24.6%; Pred. No. 2.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09503579; Patent No. 6248561

GENERAL INFORMATION:
APPLICANT: Zhang, Ning
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STRREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 RVIYQIPS--TAIAWSVYEFFKYLITKR 257
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CURRENT APPLICATION DATA: US/09/318,199
                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
                                                                                                                                                                                                                                                                                                NAME: OSMAN, RICHARD A
REGISTRATION UNDBER: 36.627
REERENCE/DOCKET NUMBER: 197-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.6'
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-09-318-199-4
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                    FILING DATE:
                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-503-579-4
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CLASSIFICATION:
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APPLICANT: Emanuel, Beverly S.
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 HIANG-----AAGCVATLLHDAAMNPAEVVKQRM------QMYNSPYHRVTDCVRAVW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 DSTRGLLCGLGAGVAEAVV---VVCPMETVKVKFIHDQTSPNPKYRGFFHGVREIVR--- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 QNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHF---NPQRRYNPSSHVLSGACAGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 VAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVG-----GVTAYFR 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 ASVFGNTPLDVIKTRMOGLE------AHKYRNTWDCGLQILKKEGLKAFYK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 RYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                     11.9%; Score 168; DB 2; Length 311; 24.2%; Pred. No. 1.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
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                                                      ATTORNEY AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELEPAX: (215) 568-3439
INFOREMETON FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/08775009 Patent No. 5935783 GENERAL INFORMATION:
                                                                                                                                                                                                                                                LENGTH: 311 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Conservative
                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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Matches 65; Conserva
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US-08-775-009-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 GVREIVR----EQGLKGTYQGLTATVLKQGSNQAIRFFVMTSLRNWYQGDNPNKPMNPLI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 HVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVG---- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDV-----IHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRM------QMYNSPYH 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 RVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHF---NPQRRYNPSS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AHKYRNTLDCGVQIL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LQPDPAA---RYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.8%; Score 166.5; DB 2; 24.7%; Pred. No. 2.6e-11; ive 35; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 KNEGPKAFYKGTVPRLGRVCLDVAIVFVIYDEVVKLLNK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---GVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 TGVFGAVAGAASVFGNTPLDVIKTRMQGLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: August 27, 2002, 03:58:51
Job time: 4893 sec
ATTORNEY AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATTON NUMBER: 35.719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACFERISTICS:
LENGTH: 311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.7%
Matches 69; Conservative
                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-775-009-3
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 27, 2002, 03:57:41; Search time 80.04 Seconds (without alignments) 318.137 Million cell updates/sec Run on:

Title: Perfect score:

US-09-870-113-8 1406 1 MQSLQPDPAARYRNVLEALW......vyeffkylitkroeewragk 265 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_71:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	tion	hypothetical prote					probable mitochond	hypothetical prote				н	PET8 protein - yea	rie				chondrial	Btl protein precur	peroxisomal Ca-dep	adenylate transloc	hypothetical prote	probable carrier p	probable mitochond	probable mitochond	hypothetical prote	peroxisomal Ca-dep		probable mitochond	probable membrane
SUMMARIES	ID	2608	T39149	S13533	A86205	S55179	T00582	T19322	S54524	T43493	696770	S44092	S45458	S54495	T20290	T09362	T01839	T01729	J01459	T50686	T05350	S64589	S57116	S62485	T40968	B96753	T49871	0	T37576	57
	DB		7	~	7	~	~	7	7	7																7	~	~	7	7
	Length	312	303	304	781	314	331	328	368	351	367	384	284	902	269	330	336	352	436	475	392	366	322	271	338	349	479	307	345	326
of	Query Match		33.2	31.4	30.7	30.4	29.4	20.1	19.6	٠.	17.7	17.2	ė.	16.0	15.6	'n	15.1	•	•		14.8	14.8	٠	•	•	14.3	•	14.2	14.1	14.0
	Score	677	467	441	431.5	428	414	283	275.5	251.5	248.5	242.5	226	224.5	219.5	216.5	213	210	209.5		208.5	208	206	0		201.5	200	199.5	g	196.5
	Result No.		7	m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2 T39149 probable RNA splicing proteinmitochondial carrier protein - fission yeast (Schizosacc C;Species: Schizosaccharomyces pombe C;Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change 17-Mar-2000

233 VIYQIPSTALAMSVYEFEKYLIT 255 ||:|:|:||||| ||:::: 283 VIFQVPATALSWSVYELFKFMLS 305

δλ g

hypothetical prote hypothetical prote	probable mitochond hypothetical prote	phosphate transpor hypothetical prote	hypothetical prote	Ca-dependent solut	probable membrane	hypothetical prote	hypothetical prote	hypothetical prote	probable mitochond	hypothetical prote	probable tricarbox	probable mitochond
D84901 T45934	T50393 T22688	T51595 T48156	B96830	T47703	S48451	T04273	S50556	S50453	T39385	T32897	T39347	T40033
0.0	7 7	2 2	~	7	7	7	~	~	7	~	~	7
358 358	335 588	309	296	332	373	325	300	335	200	650	258	277
13.9	13.7	13.4	13,3	13.2	13.2	13.2	13.1	13.1	12.9	12.8	12.7	12.7
196 193	192 191	188	187.5	186	186	185	184	184	181	179.5	179	178
30 31	33 33	34	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT T26089	7LT	1
hypo	theti	hypothetical protein W02B12.9 - Caenorhabditis elegans
C; D	te: 1	C:Species: Caemornabulits elegams C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C; AC	cessi	on: T26089
R; Sy	inbur	ne, J.; Ainscough, R.
nons A·R	feren	Submitted to the EMBL Dista Library, October 1995 A.Reference number: 220140
A; Ac	cessi	A) Accession: T26089
A;St	atus:	A;Status: preliminary; translated from GB/EMBL/DDBJ
A; MC	lecul	A; Molecule type: DNA
A; Re	sidue	S: 1-312 <wil></wil>
, A	Derim	A:Experimental source: clone W02812
C; G	C; Genetics:	
A; Ge	ne: C	A; Gene: CESP:W02B12.9
A; Ma	sod di	A; Map position: 2
A; In	trons	A;Introns: 18/3; 251/3; 286/3
C; Su	perfa	C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
ō,	ery M	atch 48.2%; Score 677; DB 2; Length 312;
Be	sst Lo tches	Best Local Similarity 50.6%; Pred. No. 7.7e-54; Matches 133; Conservative 47; Mismatches 73; Indels 10; Gaps 3;
ΟY	1	MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
qq	45	5 MOSLCPCPETKCPTPVHSLMSIVKREGWLRPLRGVNAVAAGSMPAHALYFTVYEKMKGYL 104
Qy	61	SDVIHPGGNSH-IANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQN 119
qq	105	:
QY	120	EGAGAFYRSYTTQLTMNVPFQAIHFWTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAA 179
qa	163	GVAAFYRSYTTQLAMNVPFQAIHFMSYEFWQHVLNPEHKYDPKSHLIAGGLAGGLAAAL 222
δλ	180	TTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQAR 232
1		
qq	223	TTPMDCVKTVLNTQQAAEADPANRRIFLQARYRYRGISDAVRTIYSQRGLSGFSCGLQAR 282

us-09-870-113-8.rpr

ij

Gaps

Length 304; Indels 194

254

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"Species: Arabidopsis thaliana changes: Limitatua changes are trees)
Cybecies: Arabidopsis thaliana (mouse-ear cress)
Cybate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cybates: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cybates: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cybates: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_changes, A.; Ecker, J.R.; Palm, C.J.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alon Chin, C.W.; Hughes, B.; Huizar, L.
Nature 408, 816-6820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719
A.Recession: A86205
A.Statininary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-781 <STO>
A; Cross-references: GB: AE005172; NID: 98954043; PIDN: AAF82217.1; GSPDB: GN00141
C; Genetics:
                                                                                                                                                                                                                                                 64 MISQISKISTMEGSMALWKGVQSVILGAGPAHAVYFGTYEFCKARLISPEDMQTHQPMKT 123
                                                                                                                                                                                                                                                                                                               75 GAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLT 134
                                                                                                                                                                                                                                                                                                                                             61 SDVIHPGG--NSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 NEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQE---HFNPQRRYNPSS---HVLSGACA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQAR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 GGLAAAVITPLDVVKTQLQCQGVCGCDRFTSSSI---SHVLRTIVKKDGYRGLLRGWLPR 294
                                                                                                                                                                                               15 VLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIAN 74
                                                                                                                                                                                                                                                                                                                                                                                                                         135 MNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 SLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.7%; Score 431.5; DB 2;
40.0%; Pred. No. 5e-31;
ive 35; Mismatches 104;
                                                                            31.4%; Score 441; DB 2; L. Ilarity 38.4%; Pred. No. 2.1e-32; Conservative 41; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.7%
Best Local Similarity 40.0°
Matches 104; Conservative
                                                                                                       Local Similarity
nes 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 TK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MK 303
                                                                               Query Match
Best Local S:
Matches 93,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302
                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mtRNA splice defect-suppressing mitochondrial carrier MRS4 - yeast (Saccharomyces cerevi
N-Alternate names: protein YKRO52C
C;Species: Saccharomyces cerevisiae
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jul-2000
C;Accession: S1333; S38126
R;Wiesenberger, G; Link, T.A.; von Ahsen, U.; Waldherr, M.; Schweyen, R.J.
J. Mol. Biol. 217, 23-37, 1991
A;Reference number: S13532; MUID:91108815
                                                                      A; Reference number: 221748
A; Accession: T39149
A; Residues: T-303 xcDi>
A; Cross-references: EMBL: 299168; PIDN: CAB16300.1; GSPDB: GN00066; SPDB: SPAC8C9.12c
A; Experimental source: strain 972h-; cosmid c8C9
C; Genetics:
A; Gene: SPDB: SPAC8C9.12c
A; Map position: 1
C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SALAGACAITISDAFMTPFDVIKQRWQLPSRKYKSALHCATTVFRNEGLGAFYISYPTCI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 TMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 ESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTALAWSVYEFFKYL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 NGAAGCVATLEHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 NVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-304 <VIS>
A; Cross-references: EMBL:228277; NID:9486506; PID:9486507; MIPS:YKR052c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    >
                    R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.2%; Score 467; DB 2; Length 303; Best Local Similarity 37.0%; Pred. No. 8.9e-35; Matches 90; Conservative 55; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: SGD:MRS4
A;Cross-references: SGD:S0001760; MIPS:YKR052c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: strain S288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 11R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Genome: nuclear
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9

Gaps

Indels 17; Length 781;

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probable mitochondrial carrier protein [imported] - Arabidopsis thaliana
NiAlternate names: hypothetical protein T27E13.10
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C; Accession: T00582; C84705
R; Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K submitted to the EMBL Data Library, May 1999
A; Reference number: 214178
A; Reference number: 214178
A; Reference number: 214178
A; Molecule type: DNA
A; References: EMBL, AC004165; NID:93150396; PID:93150404
A; Residues: 1-331 < ROU>
A; Cross-references: EMBL, AC004165; NID:93150396; PID:93150404
A; Experimental source: cultivar Columbia
A; Residues: 1-31 < Rounsley, S.D.; Shea, M. B; Benito, M.L.; Town, C.D.; Fujii, C.Y
M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, M. Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A; Tills: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487
A; Reserver, C.A.; Cronin, L.A.; Salzberg, S.L.; Fraser, C.M.; Venter A; Reference number: A84420; MUID:20083487
A; Reserver, C.A.; Cronin, L.A.; Salzberg, S.L.; Fraser, C.M.; Venter A; Reference number: A84420; MUID:20083487
       1;
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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A;Residues: 1-331 <STO>
A;Cross-references: GB:AE002093; NID:g3150404; PIDN:AAC16956.1; GSPDB:GN00139
                                                                                                                                                                                                                                                    : | :: | : | : | | : | | : | | : | | 309
                                                                                                               73 ANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQ 132
                                                                                                                                                                                                                                                                                                                                                  133 LTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 QESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDVIHPGG--NSHIANGAAGCVATLIHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQ 118
                                                                       RNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHI 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 S----GGNPNNSAAHAISGVFATISSDAVFTPMDMVKQRLQIGNGTYKGVWDCIKRVTR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
       5;
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       Indels
   Mismatches 109;
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       41;
       Conservative
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Best Local Similarity
Matches 102; Conserv
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A; Residues: 1-86,'S', 88-102,'L',104-127,'Y',129-141,'M',143-187,'R',189-314 <SCH>
A; Cross-references: EMBL:X06239; NID:93990; PIDN:CAA29582.1; PID:93991
A; Wiesenberger, G.; Link, T.A.; von Ahsen, U.; Waldherr, M.; Schweyen, R.J.
J. Mol. Biol. 217, 23-37, 1991
A; Title: MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new memb A; Reference number: S13532; MUID:91108815
A; Accession: S20228
A; Molecule type: DNA
A; Residues: 19-314 <WIE>
A; Residues: 19-314 <WIE>
A; Residues: 19-314 <WIE>
A; Residues: SEG12
A; Cross-references: EMBL:X56445; NID:93992; PIDN:CAA39830.1; PID:93994
B; Ratsoulou, C.; Tzermia, M.; Alexandraki, D.
submitted to the Protein Sequence Database, September 1995
A; Reference number: S56912
A; Accession: S56912
A; Accession: S56912
                                                                                                                                                                                                                                                                  mfRNA splice defect-suppressing mitochondrial carrier MRS3 - yeast (Saccharomyces cerevi N; Alternate names: protein J0675; protein YJL133w C; Species: Saccharomyces cerevisiae C; Species: Saccharomyces cerevisiae C; Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000 C; Accession: S55179; S01267; S20228; S56915; S71664 R; Katsoulou, C.; Tzermia, M.; Alexandraki, D. Submitted to the EMBL Data Library, May 1995 A; Description: The complete sequence of a 40.7 kb segment located on the left arm of yea yeast hypothetical proteins.
A; Reference number: S55159
A; Accession: S55179
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A; Residues: 1-314 <KAW>
A; Residues: 1-314 <KAW>
A; Cross-references: EMBL: 249408; NID:91008337; PID:91008338; MIPS:YJL133w
B; Katsoulou, C.; Termia, M.; Tavernarakis, N.; Alexandraki, D.
Yeast 12, 787-797, 1996
A; Title: Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X87371; NID:9854542; PID:9854563
R;Schmidt, C.; Soellner, T.; Schweyen, R.J.
Mol. Gen. Genet. 210, 145-152, 1987
A;Title: Nuclear suppression of a mitochondrial RNA splice defect: nucleotide sequence A;Reference number: S01267; MUID:88121698
A;Accession: S01267
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
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A,Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 3.3e-31;
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                                                                           295 MLFHAPAAAICWSTYEGVLY 314
                                   233 VIYQIPSTAIAWSVYEFFKY 252
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A; Residues: 1-314 <KAT>
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A; Residues: 1-314 <KAF>
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119 NEGAGAFYRSYTTQLTMNVPFQAIHFMTY-----EFLQEH-FNPQRRYNPSSHVLSG 169

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hypothetical protein DKFZp434C119.1 - human
C;Species: Homo sapiens (man)
C;Date: 21.7an.2000 #sequence_revision 21.7an.2000 #text_change 21.Jan.2000
C;Accession: T43493
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. .
submitted to the Protein Sequence Database, December 1999
A;Reference number: 222516
                                                                                                                                                                                                                                                                                                                                            EGAGAFYRSYTTQLTMNVPFQAIHFMTYE-FLQEHFNPQRR-----YNPSSHVLSGACA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 VAAVLTLPFDVVKTQRQVALGAMEAVRVNPL---HVDSTWLLLRRIRAESGTKGLFAGFL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 QNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFN---PQRRYNPSSHVLSGACAGA 174
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                              11 RYRNVLEALWRIIRTEGLWRPMRGLNVTA-TGAGPAHALYFACYEKLKKTLSDVIHPGGN 69
                                                                                                                                                                                                                                                                                                                                                                                                             SHIANGAAGCVATLLHDAAMNPAEVVKQRMQM---YNSP----YHRVTDCVRAVWQN
                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGFRSLFFGYKATLARDLPFSALQFAFYEKFRQLAFKIEQKDGRDGELSIPNEILTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 GAVAAAATTPLDVCKTLLNTQESLALNS-----HIT-GHITGMAS----AFRTVYQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTL---
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                                                                                                                                                                                                              Length 368;
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                    A,Map position: 13R
C;Superfamily: ADP,ATP carrier protein repeat homology
C;Keywords: duplication; transmembrane protein
F;50-139/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;145-241/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;253-361/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: adult testis; clone DKF2p434Cl19
                                                                                                                                                                                                           Score 275.5; DB 2;
Pred. No. 2.9e-17;
59; Mismatches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 EGVLGFFSGVGPRFVWTSVQSSIMLLLYQ 355
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28.6%;
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Best Local Similarity
Matches 75; Conserv
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-351 <AAA>
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Best Local Simi
Matches 77;
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A; Residues: 1-368 <HUN>
A; Cross-references: GB:249705; EMBL:249700; NID:9825556; PIDN:CAA89802.1; PID:9825571;
A; Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Map position: 3 //11/25/2; 179/1; 298/1 //11/20ps: 22/1; 125/2; 179/1; 298/1 //12perfamily: ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T19322
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-328 <WILL>
A; Cross-references: EMBL:246787; PIDN:CAA86739.1; GSPDB:GN00021; CESP:C16C10.1
                                                                                                                                                                                                                                                                                                                                    Species: Caenorhabditis elegans
Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YMR166c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein YM8520.15c
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Date: OB-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 29-Oct-1999
C.Accession: S54524; S54611
R.Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A.Reference number: S54510
A.Reference number: S54514
EEGFGAFYASYRTTVLMNAPFTAVHFTTYEAVKRGLREMLPEHAVGAEDEEGWLIYATAG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEKWTPPDWS--AAAVAGIVARTIAVTVVSPIEMIRTKMQSKRLTYHEIGHLVRSSMATK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GISSFYLGWTPTMLRDIPFSGIYWAGYDLFKT - NLQRRQGPDHNPFVVSFVSGAAAGVV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                   240 AAAGGLAAAVTTPLDVVKTQLQCQGVGCDRFKSSSI---SDVFRTIVKKDGYRGLARGW
                                             ACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSH-----VLSGACAGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTV----YQVGGVTAYFRGVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                              hypothetical protein C16C10.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 283; DB 2; L; Pred. No. 5.2e-18; 39; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T19924
R;Lioyd, C.
submitted to the EMBL Data Library, November 1994
A;Reference number: 219108
A;Recession: T19322
A;Accession: T19322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 RVIYQIPSTAIAWSVYEFFKYLITK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 LPRMLFHAPAAAICWSTYETVK 318
                                                                                                                                          QARVIYQIPSTAIAWSVYEFFK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Experimental source: clone C16C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.1%;
30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :Gene: CESP:C16C10.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 82
180
                                                                                                                                       230
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A.Map position: 2
A.Introns: 82.71; 113/1; 153/2; 179/2; 259/3; 359/3
A.Introns: 82.71; 113/1; 153/2; 179/2; 259/3; 359/3
C.Superfamily: Caenorhabditis probable carrier protein c2; ADP.ATP carrier protein repeat homology #status atypical <ACP1
F;4-43,141-193/Domain: ADP.ATP carrier protein repeat homology #status atypical <ACP1
F;45-67/Region: serine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nilternate names: protein N2012; protein YNL003c
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 21-Jul-2000
C;Accession: 849458; S62912; S45120
R;Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
Feast IO, 945-951, 1994
A;Title: Nucleotide sequence analysis of an 8887 bp region of the left arm of yeast c
A;Reference number: S45456; MUID:95076713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                        A;Residues: 1-384 <WIL>
A;Cross-references: EMBL:249070; PIDN:CAA88869.1; GSPDB:GN00020; CESP:T09F3.2
A;Experimental source: clone T09F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: translation not shown
A;Status: translation not shown
A;Status: 1-284 cvER-
A;Residues: 1-284 cvER-
A;Cross-references: EMBL:X77114; NID:g496710; PIDN:CAA54377.1; PID:g496713
R;Aert, R; Verhasselt, P: Voet, M.; Volckaert, G.
Submitted to the Protein Sequence Database, April 1996
A;Reference number: S62910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 HREGFKGFYKGVTASYA-GVSETMIQFCIYEYFRGVLLSDANEMDKRKMDFLNFMVAGGS 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 DVIHPGGNSHIAN----GAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 QPDPAARYRN-VLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKK--TLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-284 <AER>
A;Cross-references: EMBL:271279; NID:g1301815; PID:g1301816; MIPS:YNL003c
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 QNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQ-----EHFNPQRRYNPSSHVLSGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 AGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQV--GGVTAYFRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;201-285/Pomain: ADP,ATP carrier protein repeat homology <ACP2>F;296-381/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 17.2%; Score 242.5; DB 1; Best Local Similarity 28.3%; Pred. No. 3e-14; Matches 75; Conservative 53; Mismatches 102;
                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PET8 protein - yeast (Saccharomyces cerevisiae)
   submitted to the EMBL Data Library, April 1995
A;Reference number: Z19932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: SGD:S0004948; MIPS:YNL003c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 QARVIYQIPSTAIAWSVYEFFKYLI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 SVQLMRTVPNTAITMGTYEFVVYML 381
                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: CESP:T09F3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
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                                                                  A; Accession: T24753
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A; Molecule type: DN
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                                                                                                                                                                                                                                           C; Species: Arabidopsis thallana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Date: 02-Mar-2001
C; Date: 02-Mar-2001
C; Date: 02-Mar-2001
C; Date: 02-Mar-2001
C; M.; Edway, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Hudgas, B.; Hulzar, L.
Nature 408, 816-820, 2000
A; M.; Hulzar, L.
Nature 408, 816-820, 2000
A; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Tiller, Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable carrier protein c2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
C;Accession: S44092; T24753
R;Runswick, M.J.; Philippides, A.; Lauria, G.; Walker, J.E.
R;Runswick, M.J.; Philippides, A.; Lauria, G.; Walker, J.E.
A;Bescription: Extension of the mitochondrial transport superfamily: sequences of five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <STO>
A;Cross-references: GB:AE005173; NID:g6939230; PIDN:AAF31732.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S44092
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-384 <RUN>
A; Cross-references: EMBL: X76116; NID: 9472899; PIDN: CAA53722.1; PID: 9472900
R; Lloyd, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 HIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSP------YHRVT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 HWAHFIAGAVGDTLGSFIYVPCEVIKQRMQIQGTSSSWSSYISRNSVPVQPRGDMYGYYT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 DCVRA----VWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFN------PQRRYN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 GMFQAGCSIWKEQGPKGLYAGYWSTLARDVPFAGLMVVFYEGLKDLTDQGKKKFPQYGVN 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 PS-SHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 SSIEGLVLGGLAGGLAGGLSAXLTTPLDVVKTRLQVQGSTIKYASYKGWL----DAVGQIWRKE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 RYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.7%; Score 248.5; DB 2; Length : 28.0%; Pred. No. 8.1e-15; ive 43; Mismatches 117; Indels
                                                                                                                                                                                                                       hypothetical protein F1017.9 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 GPQGFFRGSVPRVMWYLPASALTFMAVEFLR 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 GVTAYFRGVQARVIYQIPSTAIAWSVYEFFK 251
                                       |:| || || | :: :: 317 PRIIKAAPSCAIMISTYEFGKSFFORLNOD 346
   231 ARVIYQIPSTAIAWSVYEFFKYLITKRQEE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 28.09
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: F1017.9
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hypothetical protein F23K16.90 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Gorden F23K16.90) - Arabidopsis thaliana (Mouse-ear cress) (Cipate: 11-0un-1999 #sequence_revision 11-0un-1999 #text_change 22-Oct-1999 (Cipate: 11-0un-1999 #sequence_revision 11-0un-1999 #text_change 22-Oct-1999 (Cipate: 11-0un-1999 #sevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K. submitted to the Protein Sequence Database, June 1999 A; Reference number: Z16652 A; Accession: T09362 A; Accession: T09362 A; Molecule type: DNA A; Respectations: 1-330 - ABEV> A; Cross-references: EMBL>AL078620; GSPDB:GN00062; ATSP:F23K16.90 A; Experimental source: cultivar Columbia; BAC clone F23K16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 19/1; 56/1; 85/1; 109/2; 139/3; 157/3; 189/3; 219/3; 237/1; 257/3; 284/3
                                                                                                                                                                           hypothetical protein D1046.3 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C; Accession: T20290
R; Matthews, P.
Submitted to the EMBL Data Library, December 1995
A; Accession: T20290
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: T20290
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Cross-references: EMBL: Z68160; PIDN: CAA92291.1; GSPDB: GN00022; CESP: D1046.3
A; Experimental source: clone D1046
C; Genetics:
A; Gene CESP: D1046.3
A; Mapp position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 53/2; 174/3; 226/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 RGMISVLVGSAPGAAIFFLTYKYINGQMKQVIEE--RNALVDAVSASLAEIAACAVRVPT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HFNPQR----RYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGM 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 AVANKKESGRCSPLEGAACGSVAGFIAAGLTTPLDVAKTRIMLTKN------GPAPGI 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 15.6%; Score 219.5; DB 2; 1 Similarity 26.8%; Pred. No. 2.4e-12; 61; Conservative 42; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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33.7%; Pred. No. 5.7e-12;
ilve 21; Mismatches 94.
        232 RVIYQIPSTAIAWSVYEFFKYLI 254
                                                          792 RVLRSSPQFGFTLAAYELFKGFI
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Best Local S
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 22-Oct-1999
C;Accession: S54495
C;Accession: S54495
R;Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54059
A;Reference number: S54495
A;Residues: 1-902 <BAD>
A;Residues: 1-902 <BAD>
A;Residues: 1-902 <BAD>
A;Cross-references: EMBL: Z49274; NID:9809585; PIDN: CAA89275.1; PID:9809586; GSPDB:GN0001
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable carrier protein YPR021c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YP9367.01c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                      49 RGLGSAVVASAPGASLFFISYDYMKVKSRPYISKLYSQGSEQLIDTTTHMLSSSIGEICA 108
                                                                                                                                                                                                                                                                                                                                                                                                           83 LLHDAAMNPAEVVKQRMQMY -- NSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                            CL---VRVPAEVVKQRTQVHSTNSSWQTLQSILRNDNKEGLRKNLYRGWSTTIMREIPFT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 AIHFMTYEFLQEHF---NPQRRYNPSSHVLSGACAGAVAAATTPLDVCKTLLNTQESLA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPY----HRVTDCVRAVWQN 119
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C;Keywords: mitochondrion; transmembrane protein F;1-76/Domain: ADP.ATP carrier protein repeat homology <ACPl>F;1-76/Domain: transmembrane #status predicted <TMAP. F;91-179/Domain: ADP.ATP carrier protein repeat homology <ACP3>F;91-179/Domain: ADP.ATP carrier protein repeat homology <ACP3>F;187-272/Domain: ADP.ATP carrier protein repeat homology <ACP3>
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C;Superfamily: probable carrier protein YPR021c; ADP,ATP carrier
C;Superfamily: transmembrane protein
C;Reywords: duplication; transmembrane protein repeat homology <ACP1>
F;527-615/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;724-814/Domain: ADP,ATP carrier protein repeat homology <ACP2>
                                                                                                                                                                                              Length 284;
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                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                       Best Local Similarity
Matches 66; Conserv
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Search completed: August 27, 2002, 03:57:42 Job time: 4948 sec

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OM protein - protein search, using sw model

August 27, 2002, 04:16:46; Search time 37.5 Seconds (without alignments) 273.618 Million cell updates/sec Run on:

US-09-870-113-8 1406 1 MOSLQPDPAARYRNVLEALW......VYEFFKYLITKRQEEWRAGK 265 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P22500 saccharomyc P02550 saccharomyc P00461 caenorhabdi O03829 saccharomyc Q9bzj4 homo sapien P38821 saccharomyc Q9bzj4 homo sapien Q9bzj4 homo sapien Q9bzj3 cae mays (m P53320 saccharomyc Q9834 schizosacch Q99297 saccharomyc Q10442 schizosacch Q9bzd1 homo sapien Q9dzj7 saccharomyc Q9bzd1 homo sapien Q9bzd1 homo sapien Q9dzj7 saccharomyc Q9dzj saccharomyc Q9dzj saccharomyc Q9dzj mus musculu P97521 rattus norv Q9bzz homo sapien Q9dzj homo sapien Q9dzj caenis famil Q9nzig canis famil Q9nzig canis famil Q9nzig canis famil
SUMMARIES	MRS4_YEAST WRS3_YEAST WRS3_YEAST VO51_CAEEL YN39_YEAST CG69_HUMAN EPETB_YEAST CMC2_MUUSE CMC2_HUMAN CMC1_DROME BT1_MAIZE BT1_MAIZE BT1_MAIZE BT1_MAIZE CMC2_YEAST YAD6_SCHPO MFT_HUMAN SALB_HUMAN SALB_CAREEL UCP3_CAREEL
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Score	275.283 275.283 226 226 226 227 209 209 209 209 208 208 208 208 196.5 196.5 186 187 187 187 187 187 187 187 188 186 187 187 187 187 187 187 187 187 187 187
Result No.	22

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UCP3_MOUSE TXTP_HUMAN TXTP_HUMAN TXTP_RAT TXTP_RAT TXTP_CAEEL OCP3_RAT UCP3_RAT UCP3_RAT UCP3_RAT UCP3_RAT UCP3_RAT UCP3_RAT WORD_YEAST	
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112.0 111.9 111.9 111.7 111.7 111.6 11.6	
168.5 167 165.5 165.5 164.5 164.5 164.5 163	
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REPEAT 19
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                                                                                                                                                                                                                                                                                                                                                                               GAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :: | | | | | | : : | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | 
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                         15 VLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIAN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wiesenberger G., Link T.A., von Ahsen U., Waldherr M., Schweyen R.J "MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new members of the mitochondrial carrier family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288C / FY1679;
MEDIINE=9640871; PubMed=8813765;
Matsoulou C., Tzermia M., Tavernarkis N., Alexandraki D.;
Katsoulou C., Tzermia M., Tavernarkis N., Alexandraki D.;
"Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome X reveals 14 known genes and 13 new open reading frames including homologues of genes clustered on the right arm of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            feast 12:787-797(1996).
-!- FUNCTION: MRS3 SUPPRESSES A MITOCHONDRIAL SPLICE DEFECT IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQE
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                                                                                                                                                                                                                               Score 441; DB 1; Length 304;
Pred. No. 8.3e-34;
.; Mismatches 106; Indels
                                                                                                                                             5ABBF9858B547EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1989 (Rel. 11, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MILCCHONDIAL RNA splicing protein MRS3
MRS3 OR YJL133W OR J0675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
                             POTENTIAL. POTENTIAL.
                                                                                        POTENTIAL
                                                                                                               POTENTIAL
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MEDLINE-88121698; PubMed-2448588;
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MEDLINE-91108815; PubMed=1703236;
                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                MW.
                                                                                                                                                                                                                               31.4%;
38.4%;
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                                                                                                                                             33307
                                                                                                                                                                                                                                                                                       Conservative
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  102
139
194
228
288
83
120
175
209
275
304 AA;
                                                                                                                                                                                                                                                       Best Local Similarity
Matches 93; Conserv
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P10566;
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                ITS SUPPRESSOR ACTIVITY VIA MODULATION OF SOLUTE CONCENTRATIONS THE MITOCHONDRION (POSSIBLY OF CATIONS).
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 ANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 LIMNVPFQAIHFMIYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATIPLDVCKTLLNT
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PROSITE; PS00215; MITOCH_CARRIER; 2.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                            SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. TO YEAST MRS4; BOTH PROTEINS MAY BE ISOFORMS OF THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.4%; Score 428; DB 1; Length 314; 37.2%; Pred. No. 1.4e-32;
INTRON OF THE COB GENE. IT MAY ACT AS A CARRIER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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BLOCK II (APPROXIMATE).
BLOCK III (APPROXIMATE)
POTENTIAL.
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(Rel. 35, Last sequence update)
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EMBL; X56445; CAA39830.1; ALT_INIT.
EMBL; X06239; CAA25821.1; ALT_SEQ.
EMBL; X87371; CAA60822.1; -.
EMBL; Z49408; CAA89428.1; -.
PIR; S20228; S20228.
SDD; S0023669; MRS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001993; Mitoch_carrier.
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121
213
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93
130
185
219
314 AA;
                                                                                            inner membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 SHIANGAAGCVATLLHDAAMNPAEVVKQRMQM---YNSP-----YHRVTDCVRAVWQN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 GGLAGIITTPMDVVKTRVQTQQPPSQSNKSYSVTHPHVTNGRPAALSNSISLSLRTVYQS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYRNVLEALWRI IRTEGLWRPMRGLNVTA-TGAGPAHALYFACYEKLKKTLSDVIHPGGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 EGAGAFYRSYTTQLTMNVPFQAIHFMTYE-FLQEHFNPQRR-----YNPSSHVLSGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAVAAAATTPLDVCKTLLNTQESLALNS------HIT-GHITGMAS----AFRTVYQV
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
                                                                                                                   inner membrane (Potential).
-!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOWAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
              SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
Hunt S., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
B583100018DF045D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG69_HUMAN STANDARD; PRT; 359 AA. 09BZJ4; Q9UEG6; Q9Y379; Q9PBZ; Created) 11-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Mitochondrial carrier protein CGI-69 (PRO2163).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.6%; Score 275.5; DB 1
28.6%; Pred. No. 2.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59; Mismatches
                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 GGVTAYFRGVQARVIYQIPSTAIAWSVYE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                     SGD; SO004776; YMR166C.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3_
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGVLGFFSGVGPRFVWTSVQSSIMLLLYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MM;
                                                                                                                                                                                                                                                                                                                                                                EMBL; 249705; CAA89802.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 1
260 2
368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11139402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
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                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 FRGTADAIVKIARHEGIRSLWSGLSPIMVMALPATVFYFTTYDNLSVWLKKKMCCRRAFS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 ----HPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 PEKWTPPDWS--AAAVAGIVARTIAVTVVSPIEMIRTKMOSKRLTYHEIGHLVRSSMATK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSH-----VLSGACAGAV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 AAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTV----YQVGGVTAYFRGVQA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVI----- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                    Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Mitochondrion; Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.1%; Score 283; DB 1; Length 328; 30.9%; Pred. No. 4.9e-19; live 39; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
EA1E9E329A764DF6 CRC64;
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                  Putative mitochondrial carrier C16C10.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WormPep; C16C10.1; CE01489.
InterPro; IPR001993; Mitcoh_carrier.
Pfam; PF00153; mitco.carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 RVIYQIPSTAIAWSVYEFFKYLITK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 PC
166 PC
257 PC
36743 MW;
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                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
237
328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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Q03829;
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                                                                                                                                                                                                   Lloyd C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
TRANSMEM
SEQUENCE
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PROSITE; PS00215; MITOCH_CARRIER; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional prediction of the coding sequences of 79 new genes deduced by analysis of CDNA clones from human fetal liver.", Submitted (JAN-1999) to the EMBL/GENBAN/FORD databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okamoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1/CGI-69L (shown here) and 2; are produced by alternative splicing.
-!- TISSUE SPECIFICITY: Expressed in many tissues. Abundant in testis
                               "Overexpression of the human 2-oxoglutarate carrier lowers mitochondrial membrane potential in HEK-293 cells: contrast with the unique cold-induced mitochondrial carrier CGI-69."; Biochem. J. 353:369-375(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).

Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.

Tanaka T., Nakamura Y., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
Yu X.X., Lewin D.A., Zhong A., Brush J., Schow P.W., Sherwood S.W.
                                                                                                                                                                                                                                                               TISSUE-Testis;
WEDLINE-21154917; PubMed-11230166;
WEDLINE-21154917; PubMed-11230166;
WHOMANN S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Mauber J., Duesterfoeft A., Meyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner D., Wambutt R., Gon B., Klein M., Poustka A.; Sequencing and analysis of 500 novel complete protein coding human cDNAs.";
                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Chu C.-S., Lin W.-C.;
Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and kidney.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 15-359 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORM 1).
                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF137711; AAG60687.1; -. EMBL; AF151827; AAD34064.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK026060; BAB15341.1; -. BC001398; AAH01398.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL133584; CAB63728.1; -.
                                                                                                                                                                                                             Genome Res. 10:703-713(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFC TISSUE=Brain, and Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Fetal liver
                  Pan G., Adams S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; /
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InterPro; IPR001993; Mitoch_carrier. InterPro; IPR002067; Mit_carrier.

PRINTS; PR00926; MITOCARRIER. PF00153; mito_carr;

Pfam;

BC009330; AAH09330.1; -. AF119864; AAF69618.1; -

EMBL; EMBL;

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175 VAAAATTPLDVCKT----LLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQ 230
                                                                                                                                                                                                                                                                                                                                                                 ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVW 117
                                                                                                                                                                                                                                                                                                                                                                                               156 ALTSDLYAP------MVAGALARLGTVTVISPLELMRTKLQAQHVSYRELGACVRTAV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                118 QNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFN----PQRRYNPSSHVLSGACAGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTL--- 60
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             their
                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 AQGGWRSLWLGWGPTALRDVPFSALYWFNYELVKSWLNGLRPKDQTSVGMSFVAGGISGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                     31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lalo D., Stettler S., Mariotte S., Slonimski P.P., Thuriaux P.; "Two yeast chromosomes are related by a fossil duplication of t centromeric regions.";
                                                                                                                                                                                                                                       Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95028151; PubMed-7941739;
Lalo D., Stettler S., Mariotte S., Gendreau E., Thuriaux P.;
"Organization of the centromeric region of chromosome XIV in
                                                                                                                             LPSSLQSTG -> W (IN ISOFORM 2).
                                                                                                                                                                                                                                                                     43; Mismatches 121; Indels
                                                                                                                                                       /FTId=VAR_012756.
G -> R (IN REF. 6).
952AA3DB5F5F9BD1 CRC64;
                                                                                                                                                                                                                                       17.9%; Score 251.5; DB 1; 27.8%; Pred. No. 4.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. R. Acad. Sci., III, Sci. Vie 316:367-373(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last annotation update)
Putative mitochondrial carrier protein PET8.
PET8 OR YNLO03C OR N2012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 31, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 ARVIYQIPSTAIAWSVYEFFKYLITKRQEE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 PRIIKAAPSCAIMISTYEFGKSFFQRLNQD 354
 Mitochondrion; Inner membrane; Repeat;
Alternative splicing; Polymorphism.
TRANSMEM 15 35 POTENTIAL.
                                                                POTENTIAL.
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                                                                                              POTENTIAL
                                                                               POTENTIAL
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                                                                                                                                                                          266 G
39214 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Teast 10:523-533(1994).
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235
279
338
72
72
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STRAIN-S288C / FY1679;
                                                                                                                                                                          266
359 AA;
                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                               122
161
215
215
259
318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-GRF88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995
01-OCT-1996
                                                                                                                                                                                                                                                                      75:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PET8_YEAST
P38921;
                                                                                                                             VARSPLIC
VARIANT
                                                                                                                                                                          CONFLICT
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Best Local S
                                               TRANSMEM
                                                                TRANSMEM
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                                                                                            TRANSMEM
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inasac D.S., Crackower M.A., Lee J.R., Kobayashi K., Saheki T.,
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DOMAIN
CA_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMC2_MOUSE STANDARD; PRT; 676 AA.
090XX4; 09DCF5; 09CZF6;
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier family 25, member 13) (Citrin).
            Verhasselt P., Aert R., Voet M., Volckaert G.,;
"Nucleotide sequence analysis of an 8887 bp region of the left arm of
yeast chromosome XIV, encompassing the centromere sequence.";
Yeast 10:945-951(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 LLHDAAMNPAEVVKQRMQMY--NSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 CIQFPLYEYLKKTWAKANGQSQVEPWKGAICGSIAGGIAAATTTPLDFLKTRLMLNKTTA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 AIHFMTYEFLQEHF---NPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 RGLNVTATGAGPAHALYFACYE----KLKKTLSDVIHPGG-----NSHIANGAAGCVAT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 LNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SLGSVIIRIYREEGPAVFFSGVGPRTMWISAGGAIFLGMYETVHSLLSK 274
                                                            !- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                          Inner membrane; Repeat; Transmembrane; Transport.
25 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                       inner membrane (Potential).
-!- DOMAIN: COMPOSED OF THREE HOWOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 226; DB 1; Length 284;
; Pred. No. 8.4e-14;
41; Mismatches 104; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                     761378D67DAFD343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE-20079163; PubMed-10610724;
                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                  IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
MEDLINE=95076713; PubMed=7985421;
                                                                                                                                                                                                                                                                                                                                                                                   31027 MW;
                                                                                                                                                                                                              EMBL; U02536; AA64802.1; -. EMBL; X77114; CAA54377.1; -. EMBL; Z71279; CAA55862.1; -. PIR; S45420; S45120.
                                                                                                                                                                                                                                                                                                                                                                                                                       16.1%; 27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             66; Conservative
                                                                                                                                                                                                                                                                                                                                                                        252 2
284 AA;
                                                                                                                                                                                                                                                                         S0004948; PET8
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                           Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Si
Matches 66;
                                                                                                                                                                                                                                                                                       InterPro;
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TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsudo Y., King B., Kochiwa H., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bata I., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustnocio S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mashizaki Y., Rawaji H., Kohtsuki S., Hasselawa Y., Kawaji H., Kohtsuki S., Hasselizaki Y., Rawaji H., Kohtsuki S., Hasselizaki Y., Rawaji H., Kawaji H., Kohtsuki S., Hasselizaki Y., Rawaji H., Kohtsuki S., Hasselizaki Y., Rawaji H., Kawaji H., Kohtsuki S., Hasselizaki Y., Rawaji H., Kawaji H., Kawaji
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A FUNCTION IN THE UREA CYCLE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INNER MEMBRANE (BY SIMILARITY).

-!- TISSUE SPECIFICITY: AT E10,45, EXPRESSED IN BRANCHIAL ARCHES AND LERIMB AND TAIL BUDS. AT E13.5 EXPRESSION IS PREDOMINANT IN EPITHELIAL STRUCTURES AND THE FOREBRAIN, KIDNEY AND LIVER. EXPRESSION IN LIVER IS MAINTAINED INTO ADULTHOOD.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR
Scherer S.W., Tsui L.-C.;
Genomic structure of the adult-onset type II citrullinemia gene,
SLC25A13, and cloning and expression of its mouse homologue.";
Genomics 62:289-292(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00018; EF_HAND; FALSE_NEG.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFAMILY.
-!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANCESTRAL CALCIUM SITE 3.
                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE-Embryo, and Kidney; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL). (POTENTIAL). (POTENTIAL).
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EMBL; AK012670; BAB28397.1; --
MGD; MG1:1354721; S1c25a13.
InterPro; IPR002048; EF-hand.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00036; efhand; 3.
Pfam; PF000153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
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                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
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Genomics 62:289-292(1999).
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Best Local Similarity
   8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=99295931; PubMed=10369257;
Kobayashi K., Sinasac D.S., Iijima M., Boright A.P., Begum L.,
Lee J.R., Yasuda T., Ixeda S., Hirano R., Terazono H., Crackower M.A.,
Kondo I., Tsui L.-C., Scherer S.W., Saheki T.;
"The gene mutanted in adult-onset type II citrullinaemia encodes a
putative mitochondrial carrier protein.";
Nat. Genet. 22:159-163(1999).
                                                                                                                                                                                                                                                                                                                                                                             CMC2_HUMAN STANDARD; PRT; 675 AA.
09UJS0; 09UNI7; 09NZW1; 014566; 014575;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier family 25, member 13) (Citrin).
                                                                                                                                                                                     118 ONEGAGAFYRSYTTOLTMNVPFQAIHFMTYEFLQEHF-NPQRRYNPSSHVLSGACAGAVA 176
                                                                                                                                                                        67 GCNSHI-----ANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVR----AVW 117
                                                                                                           Gaps
                                                                                                                                                                                                                                                             177 AAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQ
                                                                                                                               12 YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVI-----HP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcium-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic structure of the adult-onset type II citrullinemia gene, SLC25A13, and cloning and expression of its mouse homologue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 6-251 FROM N.A., AND DISEASE.
MEDILDE-20079163; PubMed=10610724;
Sinasac D.S., Crackover M.A., Lee J.R., Kobayashi K., Saheki T.,
Scherer S.W., Tsui L.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20115110; PubMed-10642534; Del Arco A., Agudo M., Satrustegui J.,; Characterization of a second member of the subfamily of calcium binding mitochondrial carriers expressed in human non-excitable
                                                                                                           36;
1.
2.
3.
MISSING (IN REF. 2; BAB28397).
S -> F (IN REF. 2; BAB22390).
W; 5E3952F08E5E58C5 CRC64;
                                                                                    Length 676;
                                                                                                          40; Mismatches 110; Indels
                                                                                   Score 217; DB 1;
Pred. No. 1.7e-12;
                                                      ž.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. J. 345:725-732(2000).
                                                                                   15.4%;
ilarity 27.1%;
Conservative 40
                                                     74466
                                                                                                                                                                                                                                                                                                      237 IPSTAIAWSVYEFFK 251
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 422
512
615
312
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207
423
513
312
442
676 AA;
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                                                                                   Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALCIUM-BINDING.
TISSUE-Liver;
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                               CONFLICT
                                                   SEQUENCE
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REPEAT
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                  Goela D., Hultman M., Scheet P., Cordes M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CALCIUW-DEPENDENT MITOCHONDRIAL SOLUTE CARRIER. MAY HAVE
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                          inner membrane.
-1-TISSUE SPECIFICITY: HIGH LEVELS IN LIVER AND LOW LEVELS IN KIDNEY,
PANCREAS, PLACENTA, HEART AND BRAIN.
-1-DISEASE: DEFECTS IN SICCEA13 RE A CAUSE OF ADULT-ONSET TYPE-II
CITRULLINAEMIA (CTLN2), CTLN2 IS CHARACTERIZED BY A LIVER SPECIFIC
DEFECT IN THE REGULATION OF ARGININOSUCCINATE SYMTHASE (ASS)
RESULTING IN A DEFICIENCY OF ASS. A FEW YEARS AFTER ONSET PATIENTS
ENTER A COMA AND SUFFER CEREBRAL EDEMA.
-1-MISCELLANEOUS: BINDS CALCIUM.
-1-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
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Pred. No. 4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AD07EDBC6C68989B CRC64;
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Q -> QQ (IN REF. 4).
M -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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InterPro: IPR002067; Mit.carrier.
InterPro: IPR001993; Mitoch_carrier.
Pfam; PP00036; efhand; 3.
Pfam; PP00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS0018; MITOCH_CARRIER.
PROSITE; PS0015; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EF-HAND 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y17571; CA662206.1; -
EMBL; AF164530; AAF28473.1; -
EMBL; AF164526; AAF28473.1; JOINED.
EMBL; AF164526; AAF28473.1; JOINED.
EMBL; AF164529; AAF28473.1; JOINED.
EMBL; AF164529; AAF28473.1; JOINED.
EMBL; AC002450; AAF28473.1; JOINED.
EMBL; AC002450; AAB67049.1; -
MIN; 603859; -
MIN; 603851; -
MIN; 603814; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF118838; AAD38501.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
ΜΜ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calcium-binding; Polymorphism.
SEQUENCE OF 252-675 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.18;
26.78;
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436
485
524
581
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100
139
171
207
422
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TRANSMEM
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CA_BIND
CA_BIND
DOMAIN
CA_BIND
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REPEAT
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SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Ovary;
MEDLINE=20115110; PubMed=10642534;
                                                                                                                                                                                                                                                                   142
193
313
                                                                                                                                                                                                                                                                            173
293
320 AA;
                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 62; Conserv
                                                                                                                                                                  606521;
                                                                                                                                                                                                                                                                   TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                               GGN----SHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVR----AVW 117
                                                                                    423 DGSVPLAAEILAGGCAGGSQVIF----TNPLEIVKIRLQVAG----EITTGPRVSALSVV 474
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Responsible for the uptake of deoxynucleotides into the matrix of the mitochondria. Transports all four deoxy NDPS, and, less efficiently, the corresponding dNTPs. Does not transport dNMPs, NMPs, deoxynucleosides, nucleosides, purines, or pyrimidines. Supply deoxynucleotides to the mitochondrial matrix for conversion to triphosphates and incorporation into
                      YRNVLEALWRITRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVI-----HP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dolce V., Fiermonte G., Runswick M.J., Palmieri F., Walker J.E.; "The human mitochondrial deoxynucleotide carrier and its role in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! TISSUE SPECIFICITY: Expressed in all tissues examined except for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                placenta. Highest levels in colon, kidney, lung, testis, spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                        AAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQ
                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                             01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling
  36;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bustaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Renard S., Mondesert G., Besnard F.;
"MUP 1, a mitochondrial uncoupling protein.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxicity of nucleoside antivirals.";
Proc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001)
                                                                                                                                                                                                                                                                               320 AA
 Mismatches
                                                                                                                                                                                                                                                                               PRT;
41;
                                                                                                                                                                                                                                                                                                  (Rel. 41, Created)
(Rel. 41, Last sequ
(Rel. 41, Last anno
 Conservative
                                                                                                                                                                                                 237 IPSTAIAWSVYEFFK 251
                                                                                                                                                                                                                       SPOFGVTLLTYELLO 604
                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                         SLC25A19 OR DNC OR MUP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitochondrial DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11226231;
                                                                                                                                                                                                                                                                                                  01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver
68:
                                                                                                                                                                                                                                                                                                                                                protein 1)
                                                                                                                                                                                                                                                                            DNC_HUMAN
                    12
                                                                                                                               475
                                                                                                                                                      177
                                                                                                                                                                                                                       590
Matches
                                                               67
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 DPSAKYHGILQASRQILQEEGPTAFWKGHVPAQILSIGYGAVQFLSF-----EMLTEL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| | : | | : | | | : | 107 VHRGSVYDAREFSVHFVCGGLAACMATL---TVHPVDVLRTRFAAQGEPKVYNTLRHAV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 GTMYRSEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEGKKNENLQNLLC 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 RAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFN-----PQRRYNPSSHVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACAGAVAAAATTPLDVCKTLLNT ---QESLALNSHITGHITGMASAFRTVYQVGGVTAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 320;
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nes 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.86
54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.1%; Score 212.5;
llarity 23.4%; Pred. No. 1.8
Conservative 54; Mismatches
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http://dichembor.
http:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 FRGVQARVIYQIPSTAIAWSVYEFF 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ251857; CAC27560.1; -. EMBL; AJ301616; CAC37793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF182404; AAG16903.1; -. BC001075; AAH01075.1; -. BC005120; AAH05120.1; -.
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PF00036; efhand; 3.

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                                                                                                                                                         RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gacayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Bradon R.C., Bazet R.G., Changen M., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Cawleys P.V., Barman B.P., Bhandari D., Bolshakov S.,
RA Burtis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cabriellan S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris M.L., Harvey D., Heiman T.S., Gelbart W.M., Glasser K.,
Aldek A., Goong F., Gorrell J.H., Gu Z., Kennison J.A.,
RA Harris M.L., Harvey D., Hewiann T.J., Herrandez J.R., Houtch J.,
RA Hullu K. Alush F., Karpen G.H., Ke Z., Kennison J.A.,
RA Hullu K. A., Motton C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., Muzny D.M., Nelson D.L.,
RA McHulov G., Milshma N.V., Mobarry C., Morris J., Moshreff A.,
Rabarzolo M., Pittun N.V., Mobarry C., Morris J., Moshreff A.,
Rhount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelsen M.C.,
Spier E., Spradling A.C., Stapleton M., Strong R., Pacchel T., Shen H.,
R Spier E., Spradling A.C., Stapleton M., Strong R., Standers R.,
R Spier E., Spradling A.C., Stapleton M., Strong R., Stand S., Shen K., Worley E.M., Worley E.M., Worley E.M., Worley E.M., Worley E.M., Worley E.W., Rubin G.M., Worley E.M., Worley E.M., Worley E.M., Rubin G.M., Worley E.M., Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INNER MEMBRANE (BY SIMILARITY).

-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
                     calcium.
                 "Characterization of a second member of the subfamily of calcium
binding mitochondrial carriers expressed in human non-excitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                              3).
 Arco A., Agudo M., Satrustegui J.;
Mracterization of a second member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0028646; aralarl.
InterPro; IPR002048; EF-hand.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE003774; AAF57048.1; -. EMBL; AE003774; AAF57049.1; -. EMBL; AE003774; AAF57050.2; -.
                                                                         Biochem. J. 345:725-732(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y18197; CAB62169.1; -.
                                                                                                                                  STRAIN-BERKELEY;
                                                          tissues
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | | : | | : | | : | 436 KGNIPTWAEVLAGGCAGASQVVF----TNPLEIVKIRLQVAGEIASGSKIRAWSVVREL- 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| : :::| || || || || 384 YRNSWDCFKKVVRHEGFMGLYRGLEPQLMGVAPEKA-----IKLTVNDLVRDKLTDK 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 QNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYN-PSSHVLSGACAGAVA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 AAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 ----PGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQ----MYNSPYHRVTDCVRAVW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIH----- 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN ISOFORM 3).
MHIPFPFNWIPTLPVARCQE -> LTKSLPN (IN
                                               PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00215; MITOCH_CARRIER; 3.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 210; DB 1; Length 695; Pred. No. 7.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                ANCESTRAL CALCIUM SITE 3.
                                                                                                                                                                                                                                                                                                                                                                                      GA -> AP (IN REF. 1).
V -> A (IN REF. 1).
V -> L (IN REF. 1).
9 BEC93D92031F5B77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 AA
                                                                                              Calciun-binding; Alternative splicing.
TRANSMEM 346 363 1 (POTENTIAL).
TRANSMEM 406 425 2 (POTENTIAL).
TRANSMEM 499 465 3 (POTENTIAL).
TRANSMEM 498 517 4 (POTENTIAL).
TRANSMEM 537 554 5 (POTENTIAL).
TRANSMEM 594 613 6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brittle-1 protein, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                                                          ISOFORM 2).
                                                                                                                                                                                                                             EF-HAND 2.
                                                                                                                                                                                                                                                               EF-HAND 4
                                                                                                                                                                                                                EF-HAND 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=93005685; PubMed=1668652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                        653 v
76753 MW;
Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 IPSTAIAWSVYEFFKYL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603 SPQFGVTLVTYELLQRL 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 28.0%
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                              5554
6113
1129
1168
220
627
627
524
527
52
                                 SMART; SM00054; EFh; 3
                                                                                                                                                                                                                                                                                                                                                                                         356
556
653
695 AA;
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                                                                                                                                 406
449
498
537
594
118
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P29518;
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                               CA_BIND
DOMAIN
CA_BIND
                                                                                                                                                                                                                                                                                                                                            VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                CA_BIND
                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                REPEAT
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                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
BT1_MAIZE
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SEQUENCE FROM N.A.
                                                     Frontali L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Simi
Matches 76;
                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11
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                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 VCKTLLNTQESLALNSHITGHITGMASAFRTVYQ------VGGVTAYFRGVQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 W-IMONEGWIGLFRGNAVNVLRVAPSKAIEHFTYDTAKKFLT----PKGDEPPKIPIPTP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 -IANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 TQLTMNVPFQAIHFMTYEFLQEHF-----NPQRRYNPSSHVLSGACAGAVAAAATTPLD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 LVAGALAGFASTL----CTYPMELIKTRVTIEKDVYDNVAHAFVKILRDEGPSELYRGLT
                      "Analysis of maize brittle-1 alleles and a defective Suppressor-mutator-induced mutable allele."; plant Cell 3:1337-1348(1991), el-FUNCTION: COULD PLAY A ROLE IN AMYLOPLAST MEMBRANE TRANSPORT.-1-SUBCELLULAR LOCATION: Chloroplast; amyloplast. el-TISSUE SPECIFICITY: ENDOSPERM OF DEVELOPING KERNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 WRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomyceties;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57;
Sullivan T.D., Strelow L.I., Illingworth C.A., Phillips R.L., Nelson O.E. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 436;
                                                                                                       -! - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                InterPro; irrocarr; 3.
PRINTS: PRO0153; mito_carr; 3.
PRINTS: PR001526; MITOCALCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
Transit peptide; Chloroplast; Amyloplast; Transmembrane.
TRANSIT 1 75 CHLOROPLAST (POTENTIAL).
76 436 BRITTLE-1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                       9600C05F603E9DAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%; Score 209.5; DB 1; 25.9%; Pred. No. 4.9e-12; iive 41; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VGR157C OR 69175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 ARVIYQIPSTAIAWSVYEFFKYLITKRQEE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 PSCIKLMPAAGIAFMCYEACKKILVDKEDE 419
                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                     46627 MW;
                                                                                                                                                                                                                                        EMBL; M79333; AAA33438.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Simitation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                      PIR; JQ1459; JQ1459.
                                                                                                                                                                                                                                                                                                                                                                             76
229
327
436 AA;
                                                                                                                                                                                                                                                                  MaizeDB; 47578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YG5F_YEAST
P53320;
                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
YG5F_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 HIANG-----AAGCVATLLHDAAMNPAEVVKQRMQMY-----NSPYHRVTDCVRAVW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 PIASTYPTLNPLFCGAIARVFAATSIAPLELVKTKLQSIPRSSKSTKTWMMVKDLLNETR 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 QEMKMYGPSRALFKGLETTLWRDVPPSAIYWSSYELCKERLWLDSTRFASKDANWVHF-- 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----INSFASGCISGMIAAICTHPFDVGKT--RWQISMMNNSDPKGGNRSRNMFKFLE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITG--HITGMASAFR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Succinate/fumarate mitochondrial transporter (Regulator of acetyl-CoA
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 1.
Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
                                                                                                                                                                                            inner membrane (Potential).
-!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
                         Mazzoni C., Ruzzi M., Rinaldi T., Solinas F., Montebove F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B0358B6EE818CB1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%; Score 208; DB 1; 27.4%; Pred. No. 5.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFC1_YEAST STANDARD; PRT; 322 AA. P33303; 01-FB3-1994 (Rel. 28, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X99228; CAA67613.1; -.
EMBL; Z3304.2; CAA97286.1; -.
SGD; S003489; YGR257C.
InterPro; IPR001993; Mitoch_carrier.
MEDLINE-97279233; PubMed-9133741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetase activity).
SFC1 OR ACR1 OR YJR095W OR J1921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fransmembrane; Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162
268
366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
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283 VMRVAPGQAVTFTVYEYVR 301
                                       233 VIYQIPSTAIAWSVYEFFK
                                                                                                                                                    YAD8_SCHPO
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Matches
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                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Transports tytoplasmic succinate, derived from isocitrate by the action of isocitrate lyase in the cytosol, into the mitochondrial matrix in exchange for funarate. SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial. INDUCTION: BY ETHANOL OR ACETATE AS SOLE CARBON SOURCES. REPRESSED
                                                                                                                                                                                                                                                                                                                                                                                          "Identification of the yeast ACR1 gene product as a succinate-fumarate transporter essential for growth on ethanol or acetate."; FEBS Lett. 417:114-118(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VREHLENLGIFKKNDTPKPKPLK -> RKGAFQKIWVYSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYRSYTTQLTMNVPFQAIHFMTY----EFLQEHFNPQRRYNPSSHV-LSGACAGAVAAAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCVATLLHDAAMNPAEVVKQRMQ-------MYNSPYHRVTDCVRAVWQNEGAGA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVG-----GVTAYFRGVQAR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL --- SDVIHPGGNSHIANGAA 77
                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
MEDLINE-98055465; PubMed-9395087;
Palmieri L., Lasorsa F.M., De Palma A., Palmieri F., Runswick M.J.,
                                                                                                                           Fernandez M., Fernandez E., Rodicio R.; "ACRI, a gene encoding a protein related to mitochondrial carriers, is essential for acetyl-CoA synthetase activity in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 LYRGVSLTAARQATNQGANFTVYSKLKEFLQNYH--QMDVLPSWETSCIGLISGAIGPFS
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 206; DB 1; Length 322; 26.6%; Pred. No. 7.2e-12; ive 35; Mismatches 107; Indels
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Ramezani Rad M., Kirchrath L., Hollenberg C.P.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTHQSQSH (IN REF. 1).
EC29718A0F5011A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00153; mito_carr; 3. PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001993; Mitoch_carrier
                                                                                                                                                                                                     Mol. Gen. Genet. 242:727-735(1994).
                                                                                        SEQUENCE FROM N.A. MEDLINE-94203187; Pubmed-7908717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Transport; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z25485; CAA80973.1; -. EMBL; Z49595; CAA89624.1; -. PIR; S36407, S36407, S43280; S43280. SGD; S003856; SFC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                      cerevisiae
                                                                                                                                                                                                                                                                                                                                                                            Walker J.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S:
Matches 69,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                               Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 YLQKQSNWDIS--VIAPICSALGTVVATTISTPLDIVKTRYQVATSSAMRKAEYGLQAEK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HFNPQRRYNPSSHVLSGACAG---AVAAAATTPLDVCKTLLNTQESLALNSHITG----H 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGLPISLTLITPATCLYLSTYVEAKRRFKPSV --- GEGAILYSICGMTAEVVSSFVWTPL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 RGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pran: PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 1.
Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          inner membrane (Potential).
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EF330C8CC8BDB6C4 CRC64;
                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : : | | : | | : | | : | | : | | ELGILEIAKLLFSKHGVKGFTRGLFTRMCYIMPSGMISMSVFESFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 204; DB 1; 27.0%; Pred. No. 8.9e-12; tive 41; Mismatches 110
                                                                                                update)
  ¥.
                                                                           update)
271
                                          01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence upd)
01-FEB-1996 (Rel. 33, Last annotation up Putatiye mitochondrial carrier C4G8.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001993; Mitoch_carrier.
                                                                                                                                                SPAC4G8.08.
Schizosaccharomyces pombe (Fission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z56276; CAA91209.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190
30002 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transport
STANDARD;
                                                                                                                                                                                                                                                      Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138
170
271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification in Saccharomyces cerevisiae of two isoforms of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitochondrial transporter for 2-oxoadipate and 2-oxoglutarate.";
J. Biol. Chem. 276:1916-1922(2001).
-I- FUNCTION: Transports C5-C7 oxodicarboxylates across the inner membranes of mitochondria. Can transport 2-oxoadipate, 2-oxoglutarate, adipate, glutarate, 2-oxoplutarate, oxaloacetate, citrate and malate. The main physiological role is probably to supply 2-oxoadipate and 2-oxoglutarate from the mitochondrial matrix to the cytosol where they are used in the biosynthesis of lysine and glutamate, respectively, and in lysine catabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palmieri L., Agrimi G., Runswick M.J., Fearnley I.M., Palmieri F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X92441; CHRN-L
SGD; S0005748; ODC2.
InterPro; IPR0019057; Mit.carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfan; PP00155; MITOCARRIER.
PROSITE; PS00215; MITOCARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galisson F., Dujon B.; "Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV of the yeast Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.2%; Score 199.5; DB 1; Length 24.1%; Pred. No. 2.7e-11; Live 51; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
4089082A64DBA97C CRC64;
                                                                                                 30-MAY-2000 (Rel. 39, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 11-Cochondrial 2-oxodicarboxylate carrier 2. ODC2 OR YOR222W OR YOR50-12.
   307 AA.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=S288C / FY1679;
MEDLINE=96437977; Pubmed=8840505;
                                                                  30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 E
34007 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; 275130; CAA99440.1; -. EMBL; x92441; CAA63185.1; -.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (east 12:877-885(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11013234;
ODC2_YEAST
Q99297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 62,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
SEQUENCE
   HID DATE THE SECOND OF THE SEC
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DB 1; Length 307;

71 HIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYT 130

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11 RYRNVLEALWRITRIEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNS 70

Conservative

62;

Similarity

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TOLTMNVPFQAIHF-MTYEFLQEHFNPQRRYNP-----SSHVLSGACAGAVAAAAT 180
                                                           181 TPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPST 240
                                                                                                            Search completed: August 27, 2002, 04:16:48 Job time: 1240 sec
                                                                                                                                                  241 AIAWSVY----EFFKYL 253
                                                                                                                                                                 SLMLVVFTGMMNFFRDL 303
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GenCore version 4.5

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OM protein - protein search, using sw model

Run on:
August 27, 2002, 04:19:22; Search time 130.92 Seconds
(without alignments)
350.165 Million cell updates/sec
1406
Sequence:
1 MOSLQPDPAARYRNVLEALW.......VYEFFKYLITKRQEEWRAGK 265
Scoring table:
Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5
Searched:
562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222
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Database : SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_bungi:*
4: sp_human:*
5: sp_nnvertebrate:*
6: sp_nnwmal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
15: sp_vortebrate:*
16: sp_bacteriap:*
17: sp_archeap:*
16: sp_bacteriap:*
17: sp_archeap:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q96a46 homo sapien	0920q8 mus musculu	Q969q8 homo sapien	Q9h2j3 homo sapien	homo	homo	Q9cqq7 mus musculu	Q23125 caenorhabdi	O9vay3 drosophila	094638 onchocerca	Q9nhy6 drosophila	094634 onchocerca	014281 schizosacch	Q91mj6 arabidopsis	082049 ribes nigru	064731 arabidopsis
SUMMARIES	ID	Q96A46	L 0920G8	096968	Q9H2J3	Q9NYZ2	Q9P0J2	1 090007	023125	Q9VAY3	094638	Q9NHY6	094634	014281	09LMJ6	082049	064731
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	Score	1406	1007.5	937	910	848.5	725.5	722.5	677	657.5	643	594	573	467	431.5	429.5	414
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11 0912Y0 0912Y0 0912Y0 0912P8 0912P8 0921P8 09521P8 0952175 0952175 0952175 0952175 0952175 0952175 0952175 0952175 0952175 0952175 097379	4 096CQ1 9 012482 11 0922G0 11 092FLS8 3 060029 5 018934 11 09DCF5
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280 272 273 274 275 276 276 276 276 276 276 276 276 276 276	230.5 224.5 223.5 223 223 219.5 218
111 120 130 130 130 130 130 130 130 130 130 13	2

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           181 TPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPST
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                              71.7%; Score 1007.5; DB 11; Length 338; 69.6%; Pred. No. 1.9e-90; Live 39; Mismatches 40; Indels 1;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MITOCHONDRIAL RNA SPLICING PROTEIN 3/4 (PUTATIVE MITOCHONDRIAL.
CARRIER SPLICE VARIANT).
                                                                                                                                                                                                                                                                                         LIQ. Z., Ruan Q.-G., Eckenrode S., Shi J.-D., Cruz P., Wang She J.-X.;
"A new gene which is highly expressed in NOD mice spleen.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF288621; AR28859.1; -.
SEQUENCE 338 AA; 37510 MW; BB35B1F70C56A3FE CRC64;
                                                                                                                                                                    092008;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                             338 AA
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                                                                                 241 AIAWSVYEFFKYLITKRQEEWRAGK 265
                                                                                             340 AIAWSVYEFFKYLITKRQEEWRAGK 364
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Best Local Simi
Matches 183;
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Q969G8;
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PEDGENCE FROM N.A.
MEDLIN=-21195335; PubMed=11297739;
Li F., Nikali K., Gragan J., Leibiger I., Leibiger B., Schweyen R.,
Li F., Nikali K., Gragan J., Leibiger I., Leibiger B., Schweyen R.,
Larsson C., Suomalainen A.;
"Characterization of a novel human putative mitochondrial transporter
homologous to the yeast mitochondrial RNA splicing proteins 3 and 4.";
FEBS Lett. 494:79-84(2001);
EMBL, AJ303078; CAC27997.1;
EMBL, AJ307403; AAK49520.1;
EMBL: AF327403; AAK49520.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                            89 MNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPFQAIHFMTYE 148
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Xu X., Yang Y., Gao G., Xiao H., Chen Z., Han Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF267854; AAG44723.1; -.
InterPro; IPR001993; Mitoch_carrier.
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SEQUENCE 176 AA; 19931 MW; 4A4831AC572309D4 CRC64;
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Last sequence update)
Last annotation update)
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Best Local Similarity 100.0%; Pred. No. 6.4e-84;
Matches 177; Conservative 0; Mismatches 0;
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Matches 172; Conservative
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Length 187;

DB 4;

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Page

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Query Match
Best Local Similarity 71.99
Matches 133; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                   Song H., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
Song H., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
"A novel gene expressed in human hypothalamus.";
Submitted (JAN-2000) to the EMBL/GenBank/PDBJ databases.
EMBL; AF223466; AAR64141.1;
InterPro: IPR001993; Mitoch_carrier.
Pfam; PR00153; mito_carri. 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 347 AA; 37828 MW; 700DE61B230E001E CRC64;
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Huang O., Yu Y., Huang C., Jiang C., Ren S., Zhou J., Gu
Huang O., Yu Y., Huang C., Jiang C., Ren S., Zhou J., Gu
Wang Y., Yu Y., Huang C., Han Z.;
"A novel gene expressed in human adrenal gland.";
Submitted (JUN 1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR155660; ARF674991;
InterPro; IPR001993; Mitoch.carrier.
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                                                                   Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
  347 AA
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                                       01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                         TISSUE-HYPOTHALAMUS;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                             HT015 PROTEIN.
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Best Local (
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                                                                                                                                HT015.
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Q9P0J2
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Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
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A Wynshaw Booris A., Yoshida K., Hasegawa Y., Rawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                    -SHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQ 258
                                                                                                                                         80 VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                           Gaps
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Mature 409:685-690(2001).
EMBL: AR(015770: BAB29969.1;
EMBL; AR(01575): BAB24436.1;
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                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00153; mitc_carr; 2.
PRINTS; PR00926; MITCCARRIER: UNKNOWN_1.
PROSITE; PS00215; MITCCH_CARRIER; UNKNOWN_1.
SEQUENCE 187 AA; 21194 WW; 8FB23583ABDD5E90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                    24;
51.6%; Score 725.5; DB 4 71.9%; Pred. No. 3.7e-63; ive 27; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 AA.
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
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STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
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Best Local Similarity 71.2
Matches 131; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7227;
                                                                                                                                                    01-MAY-2000
01-DEC-2001
                                                                                                 Q9VAY3;
                                                               Q9VAY3
                                                                                                                                                                                                                                                   CG4963
      RESULT
                                     29VAY3
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80 VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQLTMNVPF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 QAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQESLALN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDVIHPGGNSH-IANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                    |:|||:||||||| ||:||| ||::|| ||::|| ||::|| ||::||| ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::
                                                                                                                                                                                                                                                                         200 -SHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLITKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 TTPLDVCKTLLNTQESLALNS-----HITGHITGMASAFRTVYQVGGVTAYFRGVQAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Swinburne J., Ainscough R.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
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EMBL; Z66521; CAA91399.1; -.
EMBL; Z66521; CAA91399.1; -.
EMBL; PF00153; mito_carrier.
Pfam; PF00153; mito_carr; 3.
PR051FE; P800215; MITOCH_CARRIER; UNKNOWN_2.
PR051FE; P800215; MITOCH_CARRIER; UNKNOWN_2.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Mismatches
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Matches 133; Conservative
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Q23125;
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                                                                                                                                 280 IIFQIPSTALSWSAYELCKYMLS 302
                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL 41.8 KDA PROTEIN.
                                                                                                          VIYQIPSTAIAWSVYEFFKYLIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.2%
Best Local Similarity 47.5%
Matches 121; Conservative
                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 TAIAWSVYEFFKYLI 254
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269 TAICWSTYEFFKFYL 283
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                          TPLDVCKTLLNTQES-
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01-FEB-1997 (
01-FEB-1997 (
01-JUN-2001 (
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01-JUN-2001
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                                                                                                                                                                                                                                                             9 XHN 60
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Blochim. Blochys. Act 1282:179-181(1996).
EMBL: U45998; AAB19037.1;
Interpro; IPR001993; Mitoch_carrier.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 303 AA; 33861 MW; 224BFA547E5D617C CRC64;
                                                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 AKFTSVRNLNYVISGA -- - VATLIHDAISSPTDVIKQRMQMYNSPYTSVVSCVRDIYKRE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 LØSLCPCPETSCPTAMHSLMSMVKREGLLRSLKGVNAVVLGTIPAHAFYYTVYENSKAYL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 LN--NPRVSNSVSYAISGALATVIHDAVMNPAEVVKQRMQMIFSPYGNSLECIRCIYIRE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
NCBI_TaxID=6282;
                                                                                                                                                                                                                                     1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
                                                                                                                                                                                                                                                                42 MQSL--SPPTKNMNIVSTLRTMITREGLLRPIRGASAVVLGAGPAHSLYFAAYEMTKELT
                                                                                                                                                                                                                                                                                                                         SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPST
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Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 379 AA; 41794 MW; F6A20BABA35F5C2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02, Last sequence update)
17, Last annotation update)
                                                                                                                                                     DB 5;
                                                                                                                                                46.8%; Score 657.5; DB 5;
llarity 51.2%; Pred. No. 4.5e-56;
Conservative 35; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.7%; Score 643; DB 5;
46.4%; Pred. No. 8.7e-55;
Live 48; Mismatches 83;
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Best Local Similarity 46.4
Matches 122; Conservative
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                                                                                                                                                                       al Similarity
130; Conserv
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01-FEB-1997
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Best Local S
Matches 130
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                               ::::|| ||||:||| ::: AKFTSVRNLNYVISGA---VATLIHDAISSPTDVIKTAYADCTTRPTHPVVSCVRDIYKR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQR-MQMYNSPYHRVTDCVRAVWQN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 MQSL--SPPTKNMNIVSTLRTMITREGLLRPIRGASAVVLGAGPTHSLYFAAXEMTKELT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 EGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAA
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Schmid K.J., Tautz D.;
Schmid K.J., Tautz D.;
A screen for rapidly evolving genes from Drosophila.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF217402; AAF73387.1;
FlyBase; FB901039561; CG4963.
InterPro; IPR001993; Mitcoh_carrier.
InterPro; IRR020667; Mit_carrier.
Pfam; PF00153; mitco_carrier.
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380 Aa; 41844 MW; 4C9AA524B97F8C6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last annotation update)
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47.5%; Pred. No. 7.5e-50;
tive 35; Mismatches 85;
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F10K1.26 PROTEIN. F10K1.26.
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                                                                                         P SEQUENCE FROM N.A.

RA Catmull J., Miller D.J.;

RA Catmull J., Miller D.J.;

RT "cnDNs from Onchocarca sp. encoding members of the MRS3/MRS4 class of mitochondrial solute carriers.";

RL Biochim. Biophys. Acta 1282:179-181(1996).

BE EMBL: U45997; AABLE 100.1.

BR FIGHT: PR001993: Mitoch_carrier.

BR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TPLDVCKTLLNTQESLALNSHI-----TGHITG-------MASAFRTVYQVGGVTA 224
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Onchocerca gibsoni.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                               ; Score 573; DB 5; Length 301;
; Pred. No. 6.3e-48;
45; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - FRGLQARIIFQVPSTALSWSAYELCKYMLS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last annotat PUTATIVE MITOCHONDRIAL CARRIER C8C9.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                 40.8%;
MITOCHONDRIAL SOLUTE CARRIER
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 43.9%
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                         NCBI_TaxID=6284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        014281;
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Liu S.X., Chan A. Yu G., Etgu P., Lee J.M., Lenz C., Pham P.,
Sakano H., Toriumi M., Chung M., Goldsmith A., Liu A., Liu A.,
Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,
Conway A., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B.,
Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
Ecker J.R., Federspial N.A., Theologis A.;
"The sequence of BAC Flok! from Arabidopsis thaliana chromosome l.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC06791: AARS217.1;
InterPro; IPR001993; Mitoch.carrier.
                                                                                                                                                                                                                                                                                                                                             60 NIVNSVIKISSTEGVYSLWRGISSVIMGAGPSHAIYFSVLEFFKSK----INASPDRPLA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                74 NGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTQL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 TMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVLSGACAGAVAAAATTPLDVCKTLLNTQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 MQALRPCP-LKPVGIREAFRSIIQKEGPSALYRGIWAMGLGAGPAHAVYFSFYEVSKXYL 122
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                               14 NVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIA 73
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9
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                                                                                                                                                                                                            Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 431.5; DB 10; Length; Pred. No. 1.7e-33; 35; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00153; mito_carr; 4.
PRINTS; PR00926; MITOCARRIER:
PROSITE; PS00215; MITOCH_CARRIER: UNKNOWN 2.
SEQUENCE 781 AA; 87081 MW; 9FB579B9BD746D1E CRC64;
                                                                                                                              69975CDE18107AB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                         33.2%; Score 467; DB 3;
37.0%; Pred. No. 1.6e-37;
iive 55; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            781 AA
                        POTENTIAL. POTENTIAL.
                                                                           POTENTIAL. POTENTIAL.
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POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                 MM.
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40.0%;
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                                                                                                                                 32652
                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
32
101
137
184
228
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Best Local Similarity
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Woodhead M.R., Taylor M.A., Brennan R.M., McNicol R.J., Davies H.V.;
Woodhead M.R., Taylor M.A., Brennan R.M., McNicol R.J., Davies H.V.;
"Cloning and characterisation of the cDNA clones of five genes that
are differentially expressed during ripening in the fruit of
Dlackcurrant (Ribes nigrum L.).";
"Blackcurrant (Ribes nigrum L.).";
"Submitted (JUN-1998) to the EMBL/Genbank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTERRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELOMGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AJ007580; CAA07568.1;
-.- SIMILARITY: BELOMGS TO THE MITOCHONDRIAL CARRIER FAMILY.
REMBL; AJ007580; CAA07568.1;
-.- SIMILARITY: BELOMG TO THE MITOCHONDRIAL CARRIER FAMILY.
REMBL; AJ007580; CAA07568.1;
-- SIMILARITY SIMICOCHONDRIAL CARRIER;
REMBL; AJ007580; CAA07568.1;
-- SIMILARITY SIMICOCHONDRIAL CARRIER;
REMBL; AJ007580; CARL: 3.
R PROSITE; PS00215; MITOCH_CARRIER; 2.
R Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 289 AA; 30383 MW; 5666EAB03DCC507C CRC64;
                                                                                                                                     172
                                                                                                                                                                                                         237
                                                                                                                                                                                                                                                                                                                                               294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDVIHPGG--NSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQ 118
                                       173 GAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQAR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 NSHIANGAAGCVATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTTQLTMNVPFQAIHFMTYEFLQE---HFNPQ--RRYNPSSHVLSGACAGAVAAATTPL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 DVCKTLLNTQESLALNSHITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                              119 NEGAGAFYRSYTTQLTMNVPFQAIHFMTYEFLQE---HFNPQRRYNPSS---HVLSGACA
                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Saxifragales; Grossulariaceae; Ribes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289
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STRALN-CV. BEN ALDER; TISSUE-FRUIT;
Woodhead M.R.;
Thesis (1995), University of Dundee, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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01-NOV-1998 (TTEMBLIEL: 08, CT-
01-NOV-1998 (TTEMBLIEL: 08, La.
01-DEC-2001 (TTEMBLIEL: 19, La.
MITOCHONDRIAL CARRIER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                   233 VIYQIPSTAIAWSVYEFFKY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Search completed: August 27, 2002, 04:19:23 Job time: 1290 sec

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06-APR-2000; 2000WO-US09534
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18-AUG-1999;
12-NOV-1999;
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502
1 MOSLQPDPAARYRNVLEALW......GAAGCVATLLHDAAMNPAEG
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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	Description	Human uncoupling p	Human transport pr	Human polypeptide	Human polypeptide	Human protein SEQ	Human ORFX ORF2744	Human mitochondria	Human bone marrow	Novel human secret	Human ORFX ORF2730	Drosophila melanog
		, , , , ,										
	П	AAB50383	AAB60113	AAM41505	AAM39719	AAM79039	AAB42980	AAB60658	AAM00938	AAU29748	AAB42966	ABB61130
		21	22	22	22	22	21	22	22	22	21	22
	Query Match Length DB	289	289	318	268	299	272	331	366	677	155	379
æ	Query	98.8	98.8	98.8	93.0	70.1	6.69	6.69	6.69	64.1	55.0	34.2
	Score	496	496	496	467	352	351	351	351	322	276	171.5
	Result No.	1	7	3	4	S	9	7	80	6	10	11

Soppet DR;

Ni J, Komatsoulis G, Rosen CA,

Ruben SM,

(HUMA-) HUMAN GENOME SCI INC

99US-0128701. 99US-0142821. 99US-0149448. 99US-0164751.

Human immune/haema Blackcurrant RIB7 Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Human bone marrow Drosophila melanog Human protein sequ	Human polypeptide Human polypeptide Human polypeptide Arabidopsis thalia Human uncoupling p Human nocupling p Human protein SEQ Human polypeptide Human polypeptide Human polypeptide Human polypeptide Human secreted pro Drosophila malanog Wheat brittle-1 pa	ve; antiarthritic; ; vasotropic; ceriai; opthalmological; ical; vulnerary; thrombolytic; sease; thrombosis; arthritis;
AAM85891 AAW17054 AAG43094 AAG22079 AAG22077 AAG43092 AAG43092 AAG43092 AAB69108 AAB69108	AAM39173 AAM40959 AAM40959 AAG19645 AAG50519 AAG7172 AAG7171 AAG7171 AAG7171 AAM50319 AAM50319 AAM50319 AAM42411 AAM42413 AAM42413 AAM42413 AAM51195 AAM51142 AAM51142	ALIGNMENTS T. 1 383 AAB50383 standard; Protein; 289 AA. AAB50383; 12-MAR-2001 (first entry) Human uncoupling protein #6. Human; uncoupling protein; immunosuppressive; antiarth antirheumatic; antiproliferative; cardiant; vasotropic cerebroprotective; muroprotective, antibacterial; optigaen therapy; cancer; wound; infectious disease; throminfertility. WO200061614-A2.
559 778 778 331 331 113	311 22 374 237 237 237 228 241 268 27 288 211 288 211 211 228 211 238 211 211 211 211 211 211 211 21	rd; Protein; 289 irst entry) g protein #6. ng protein; immu antiproliferativ ve; neuroprotect l; nephrotropic; ancer; wound; in
	19.0 19.0 19.0 18.8 18.8 18.8 18.8 19.8 10.7 17.7 17.7 17.7 17.7 17.7 17.7 17.7	883 standard; Prote 883; <pre> </pre> <pre> <pre> %-2001 (first entr. uncoupling protein eumatic; antiproli proteitive; neuro protective; neuro intestinal; nephro cherapy; cancer; wo illity. sapiens. %-2000. </pre></pre>
1367 1308 111111109999	@ @ @ @ @ @ @ @ @ @ @ @ @ @ @ @ @	T. 1 383 AAB50383 standar AAB50383; 12-MAR-2001 (fi Human; uncoupling antirheumatic; a cerebroprofectiv gastrointestinal gene therapy; ca infertility. Homo sapiens. HOMO Sapiens.
222222222222222222222222222222222222222	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT AAB50383 XX AAC AAB AC AC AAB AC AC AAB AC

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Gaps

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Indels

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The present invention provides the protein and coding sequences for 43 novel human transport proteins (designated TPPTs). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                   1 MQSLQPDPAARYRNVLEALWRIRTEGLWRPWRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                25 mqslqpdpaaryrnvlealwriirteglwrpmrglnvtatgagpahalyfacyeklkktl 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating disorders
                                                                                                                                                                                                  Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qian XB,
Yang Y,
                                                                                                                                                                                                 98.8%; Score 490; 22.100.0%; Pred. No. 4.4e-54; Live 0; Mismatches 0;
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Xu C, Xue AJ,
;, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 6436; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                    SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                 Claim 2; Page 133-134; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 6436.
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Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM41505 standard; Protein; 318
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0654450.
2000US-0662191.
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2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                    Query Match 98.8
Best Local Similarity 100.
Matches 93; Conservative
                                                                                                                      disorders such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-442253/47.
N-PSDB; AA160661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang Z, W
Zhou P,
                                                                                                                                                     289 AA;
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19-OCT-2000;
29-NOV-2000;
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09-JUL-2000;
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03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000;
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β,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM41505;
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                                                                                                                                                The present sequence is a human uncoupling protein. The nucleotide sequences encoding the uncoupling proteins may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptide with a human transport protein sequence is useful for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular systems -
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                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Uncoupling proteins and nucleic acid sequences encoding them, usefu for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders -
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                                                                                                                                                                                                                                                                                                                                                                      Length 289;
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Patterson C;
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                                                                                                                                                                                                                                                                                                                                                                  Score 496; DB 21;
Pred. No. 4.4e-54;
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u DAM, Au-Young J, P
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                 Claim 11; Page 323-324; 343pp; English
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                                                                                                                                                                                                                                                                                                                                                      98.8%; Scc.
100.0%; Pred
0; N
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99US-0148177.
99US-0149357.
99US-0162287.
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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2000-656322/63
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                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                 N-PSDB; AAC90457
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10-AUG-1999;
18-AUG-1999;
28-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                  93;
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                                                                                                                                                                                                                                                                                                                     Sequence
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Best Local
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AAB60113

Best Loc Matches

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Ren F, W Zhang J;

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WPI; 2001-442253/47.
N-PSDB; AAI58875.
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20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                 specification
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20-JUN-2000;
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01-SEP-2000;
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                    immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Latelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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                                                                                                                                                            The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ren F, Wang D;
                                                                                                                                                                                                                                                                                       The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                            1 MOSLOPDPAARYRNVLEALWRITRTEGLWRPWRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang J;
                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                               98.8%; Score 496; DB 22; Length 318; 100.0%; Pred. No. 4.9e-54; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang Y,
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Xu C, Xue AJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO 2864.
                                                                                                                                                                                                                                                                                                                                                                                                    AAM39719 standard; Protein; 268
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Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
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03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-06534519.
19-GCT-2000; 2000US-0653036.
29-NOV-2000; 2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-2001 (first entry)
                                                                                                                                                                                                                   Query Match
Best Local Similarity luv...
And 93; Conservative
                                                                                                                                                                                             318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200153312-A1.
                                                                                                                                                                      specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-2000;
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09-JUL-2000;
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Wang J, V
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leukaemia
                                                                                                                                                                                               Sequence
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-brager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and C.N.S. disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 467; DB 22; Length 268;
Pred. No. 1.8e-50;
0; Mismatches 5; Indels (
                                                                                               Example 4; SEQ ID NO 2864; 10078pp; English.
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94.6%;
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2000US-0560875.
2000US-05208075.
2000US-0620325.
2000US-0654936.
2000US-0633251.
2000US-063325.
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Best Local Similarity 94.6
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 AA;
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0
                                                                                                                                                                                           The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopoiesis regulating activity, issue growth factor activity, immunomodulatory activity and activity in activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vulnerary; antipsoriatic; antiparkinsonian; notropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunosuppression; neuroprotective; anticonvulsant; thrombolytic; coagulant; vasorropic; antidabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation;
                            Υ;
                                                                                                                                                                                                                                                                                                                           treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                      Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAW80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                              Жa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MOSLQPDPAARYRNVLEALWRITRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                             Cao Y,
                       Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Yang Y, Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ORFX ORF2744 polypeptide sequence SEQ ID NO:5488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.1%; Score 352; DB 22;
68.8%; Pred. No. 6.6e-36;
ive 12; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 ndvfhhqgnshlangiagsmatllhdavmnpae 192
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                                                                                                                                                                     Claim 20; Page 4043; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB42980 standard; Protein; 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2001 (first entry)
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Best Local Similarity 68.88
Matches 64; Conservative
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                                                                                 WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                 299 AA;
(HYSE-) HYSEQ INC
                                                                                               N-PSDB; AAK52172
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                                                                                                                                                                                                                                                                                                                                           inflammation
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                            rang YT,
                                         Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                      Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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AAL/140 to encode the proteins given in AAB1023, to AAAI/100 encode the proteins given in AAAI/100 encode the proteins given in AAAI/100 encode the human ORFX open reading frames 1 to 3161. Understy, sequences have activities such as: cytostatic; hepatotropic; vulnerary; orticopathic; anticonvulsant; antiarthritic; immunosuppressant; immunosuppressant; immunosuppressant; immunosuppressant; antidabetic; hypotensive; dermatological; immunosuppressive; antidabetic; hypotensive; dermatological; antimunosuppressive; antidabetic; hypotensive; dermatological; antiviral; antifungal; antirhematic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or traating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy or ectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allestes, antilitagementation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human mitochondrial solute carrier protein; hMSC\text{-}o;\ hypothalamus;\ preparation;\ detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.9%; Score 351; DB 21; Length 272; 67.7%; Pred. No. 7.9e-36; Live 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human mitochondrial solute carrier protein hMSC-o.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 4662-4663; 5507pp; English
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                                                                                                                                                                          990S-0127636.
990S-0127728.
20000S-0540763.
                                                                       31-MAR-2000; 2000WO-US08621
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                                                                                                                                                                                                                                                                                                                                                                                                 Leach M;
                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                     30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                     Shimkets RA,
                                                                                                                                                                                 02-APR-1999;
05-APR-1999;
                                                                                                                                               31-MAR-1999;
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05-OCT-2000
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Best Local 3
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Tue Aug 27 07:53:45

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The present sequence is one of 251 novel human polypeptides encoded by a bone marrow-expressed polynuclectide. The polynuclectide and the polypeptide encoded by it are useful in the treatment of various in polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation infection, or may result from an autoimmune disorder, a coagulation suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease, Detection of the presence or increased expression of the polynuclectide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynuclectide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                            Novel bone-marrow-expressed polynuclectides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                         Liu C, Asundi V, Chen R, Ma )
I C, Xue AJ, Yang Y, Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.9%; Score 351; DB 22;
67.7%; Pred. No. 1.1e-35;
ive 13; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 504-505; 648pp; English.
                                                                                                                                     Boyle BJ, Tang YT, Liu (
ang J, Werhman T, Xu C,
Zhou P, Drmanac RT;
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03-AUG-2000; 2000US-0653450
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
30-NOV-2000; 2000US-0250583.
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                                                                                                                                                                                                                  WPI; 2001-488707/53.
N-PSDB; AAH90057.
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Best Local Similarity
Matches 63; Conserv
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                                                                                                    (HYSE-) HYSEQ INC.
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                                                                                                                                                             Wang
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                                                                                                                                                           Ren F, Wa
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                         Ford JE,
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                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel human mitochondrial solute carrier protein, hMSC-o (AAB60658), and cDNA encoding it (AAF59920). hMSC-o is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-o proteins and nucleic acids, and the detection of hMSC-o proteins and nucleic acids, and the sequence represents hMSC-o.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                       New human mitochondrion solute carrier protein and its nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 331;
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Pred. No. 1e-35;
3; Mismatches 17; Indels
                                                                                                                                                                                                                    (SREN-) SOUTHERN RES CENT NAT HUMAN GENE GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 20; 21pp; Chinese.
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2000US-0552317.
2000US-0598042.
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                                                                                                                                                                                                                                                       Gao X, Xiao H;
                                                                                                                                                                                                                                                                                              WPI; 2001-050544/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 AA;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                    Homo sapiens
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                                                           CN1269409-A.
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Length 366; Indels us-09-870-113-10.rag

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                                                                                                                                                                                                      polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides we cettors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUS310-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
W vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
W nulsconvulsant; osteopathic; antiarthitic; immunosuppressant; cardiant;
W munostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic;
W hypotensive; dermatological; immunosuppressive; antidiabetic;
W antiviral; antibacterial; antifungal; antifunematic; antidiabetic;
W antianaemic; gene therapy; cancer; proliferative disorder; hypotrension;
W antidiovascular disease; diabetes mellitus; hypothyroidism; SCLD; ALDS;
Cholesterol ester storage; systemic lupus erythematosus; infection;
severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
M allergy; aphastic anaemia; nocturnal haemoglobinuria; burn; wound;
W thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                              invention relates to novel human secreted polypeptides. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.1%; Score 322; DB 22; Length 677; 63.4%; Pred. No. 1.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX ORF2730 polypeptide sequence SEQ ID NO:5460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                Claim 20; Page 189; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB42966 standard; Protein; 155 AA.
                                                          Liu C, Drmanac RT
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2001 (first entry)
                                                                                     WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  677 AA;
                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                         rang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB42966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabatic; hypotensive; dermatological; immunosuppressive; antidiabatic; hypotensive; dermatological; annunosuppressive; antithyroid; and antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
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Pred. No. 1.1e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 4641; 5507pp; English.
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                                                                                                                                        31-MAR-2000; 2000WO-US08621.
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133 ndvfhhqgnshlang 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leach M;
                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
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Best Local Similarity
Matches 48; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-602362/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAC77175
WO200058473-A2.
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                                                                                                                                                                                                            31-MAR-1999;
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                                                                    05-OCT-2000
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ABB61130
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17-JAN-2001; 2001WO-US01354
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30-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
14-SEP-2000;
25-SEP-2000;
25-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

(ABB57737-ABB72072).

(ABB57737-ABB7 for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.2%; Score 171.5; DB 22; Length 379; 40.9%; Pred. No. 5.2e-13; Live 16; Mismatches 34; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 10182; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen SEQ ID NO:13484
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100 akftsvrnlnyvisga---vatlihdaissptd 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                Myers EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM85891 standard; Protein; 59 AA
                                                                                                                                                                                                                                                Li PWD,
                                                                                                                                      23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Conservative
                                            Drosophila melanogaster
                                                                                                                                                                                                                                              Venter JC, Adams M,
                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                  (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 AA;
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                                                                         WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                     interactions -
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                                                                                                        27-SEP-2001
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
cample, they may be used to treat disorders associated with decreased
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
concers and cancer human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK54950 and AAM82169
represent sequences used in the exemplification of the present invention. ij Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and RIB polypeptides (AAW17050-54) are encoded by cDNA clones (AAT68953-8 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHP 66 New isolated promoters from blackcurrant fruit - used for driving fruit-specific expression of DNA sequences in transgenic blackcurrant and other non-climacteric fruit Claim 11; SEQ ID NO 13484; 3071pp + Sequence Listing; English. Blackcurrant; fruit-specific promoter; RIB7; transgenic plant. 33.0%; Score 165.5; DB 22; Length 59; 59.3%; Pred. No. 2.8e-13; Live 1; Mismatches 12; Indels 11. ,8e-13; .as 12; Indels Brennan RM, Taylor MA, Woodhead MR; Example 4; Page 35-36; 66pp; English AAW17054 standard; Protein; 289 AA (SMIK) SMITHKLINE BEECHAM PLC. Blackcurrant RIB7 polypeptide Ribes nigrum strain Ben Alder 96WO-EP04807 95GB-0022558 (first entry) Conservative WPI; 1997-281041/25. N-PSDB; AAT68957. Best Local Similarity Matches 35; Conserv 59 AA; W09717452-A1 04-NOV-1996; 03-NOV-1995; 05-AUG-1997 15-MAY-1997. metastasis AAW17054; Sequence Query Match g ò

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990S-0135124.
990S-0135353.
990S-0135629.
990S-0136021.
990S-0136392.
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990S-0137528.
990S-0137502.
990S-0138094.
990S-0138847.
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990S-0141287
990S-0141287
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990S-0142390
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990S-0143542
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99US-0144085.
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99US-0144325.
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99US-0144332.
99US-0144333.
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99US-0144632.
99US-0144884.
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                20-MAY - 1999;
24-MAY - 1999;
25-MAY - 1999;
25-MAY - 1999;
27-MAY - 1999;
01-JUN - 1999;
01-JUN - 1999;
04-JUN - 1999;
06-JUN - 1999;
06-JUN - 1999;
16-JUN - 1999;
16-JUN - 1999;
16-JUN - 1999;
18-JUN - 1999;
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22 - 70N - 1999

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16-JUL-1999;
16-JUL-1999;
19-JUL-1999;
19-JUL-1999;
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12-JUL-1999;
13-JUL-1999;
14-JUL-1999;
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20-JUL-1999;
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                                                                                                                                                                                Gaps
                                                                                                                                                                                                                             9 AARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG 68
57) that exhibit differential expression in blackcurrant fruit during the ripening period of fruit development. RIB7 shows case similarity to yeast MRS4, a yeast mitochondrial RNA splicing protein. RNA is expressed almost entirely in fruit. The promoter region (AAT68952) of the RIB7 gene can be used as a fruit-specific promoter.
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                                                                                                                                                Query Match 26.0%; Score 130.5; DB 18; Length 289; Best Local Similarity 35.3%; Pred. No. 5.5e-08; Matches 30; Conservative 17; Mismatches 35; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                          AAG22079 standard; Protein; 278 AA.
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990S-0123180.
990S-0123548.
990S-0125788.
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US-09-068-140A-10

US-09-068-140A-10

Sequence 10, Application US/09068140A

Fatent No. G281409

GENERAL INFORMATION:
APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
APPLICANT: Mary Rose Moodhead, Mark Andrew Taylor
APPLICANT: Aing of Prussia
COMPUTER READABLE FORM:
STREET: 709 Swedeland Road
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BENEVER COMPUTER: BENEVER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BENEVER COMPUTER: BENEVER COMPUTER:
MEDIUM TYPE: Ploppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: READABLE FORM:
CLASSIFICATION NUMBER: US/09/068,140A
FILING DATE: NO. 6281409ember 4, 1996
APPLICATION NUMBER: 33,680
FILING DATE: NO. 6281409ember 4, 1996
APPLICATION NUMBER: 33,680
FREERENCE/COCKET NUMBER: 33,680
FREERCH FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 anino acids
TYPE: anino acid
TYPE: anino acid
TYPE: NOT ANINOW
TOPOLOGY: UNKNOWN
TOP
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                                      69 NSHIANGAAGCVATLLHDAAMNPAE 93
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amino acid
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                                    ; Score 130.5; DB 4; Length 289;
; Pred. No. 1.5e-08;
17; Mismatches 35; Indels 3
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                                                                                                                                                                                                                                                                                                              Sequence 15, Application US/09068140A
Patent No. 6281409
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
APPLICANT: and Rex Michael Brennan
TITLE OF INVENTION: Blackcurrant Promoters and Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: NO. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             :: |: :| || :| :| 89 SNSGAHAVSGVFATVASDAVITPMD 113
                                                                                                                                                                                        69 NSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
TELEFAX: 610-270-5019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
                                    26.0%;
ilarity 35.3%;
Conservative 17
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE: peptide
HYPOTHERICAL: YES
ANTI-SENGE.:
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CRIGINAL SOURCE:
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STRAIN: Ben Alder
US-09-068-140A-15
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STRANDEDNESS: un}
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CLASSIFICATION:
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92 DP-TRFTGTMDAFVKIVRHEGTRTLM---SGLPATLVMTVPATAIXFTAXDQLKAFLCGR 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.8%; Score 89.5; DB 2; Length 351; Best Local Similarity 32.3%; Pred. No. 0.0029; Matches 31; Conservative 12; Mismatches 32; Indels 21;
                                                                                                                                                                                                                                                                                                                  APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 ALTSDLYAP------MVAGALARLGTVTVISPLE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF-0356 US
                                                                                                                                     Sequence 19, Application US/08933750C; Patent No. 5932442; GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L. APPLICANT: Bandman, Olga APPLICANT: Shah, Purvi
NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
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9 AARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG 68

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Ouery Match 17.7%; Score 89; DB 2; Length 320;
Best Local Similarity 27.3%; Pred. No. 0.0029;
Matches 24; Conservative 18; Mismatches 28; Indels 18; Gaps
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APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neal C.
TILLE OF INVENTION: HOWAN REGULATORY MUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incuto
                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 97,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                 ADDRESSEE: Incree Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304 COMPUTER READALE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 VHRGSVYDAREFSVHFVCGGLAACMATL 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
Shah, Purvi
Au-Young, Janice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 320 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SPLNNOT02
; CLONE: 207452
US-08-933-750C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                        APPLICANT: Lal, Preeti
APPLICANT: Hilman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 ALTSDLYAP------MVAGALARLGTVTVISPLE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMFUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION:
TELEFAX: 415-845-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-933-750C-12; Sequence 12, Application US/08933750C; Patent No. 5932442; Extent No. 5932442; GENERAL INFORMATION:
                                                           Sequence 19, Application US/09234613 Patent No. 6132973 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 32.38
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LIBRARY: SYNOOAT01
; CLONE: 724157
US-09-234-613-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                    US-09-234-613-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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TOPOLOGY: linear
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US-08-936-135-4
Sequence 4, Application US/08936135
Fatent No. 6054319:
GENERAL INFORMATION:
APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: He, Zhigang
TITLE OF INVENTION: Semaphorin Receptors
UNMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
COUNTRY: USA
ZIP: 94010
APPLICANT: Guegler, Karl J.

APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 89; DB 4;
; Pred. No. 0.0029;
18; Mismatches 28
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILLING DATE: September 23, 1997
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---NSH-IANGAAGCVATL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.78; 27.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
| IMMEDIATE SOURCE:
| LIBRARY: SPLNNOT02
| CLONE: 207452
| US-09-234-613-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 IHPGG----
                                                                                                                                                                               94304
                                                                                                                                                S
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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MEDIUM TEPE: Indepy disk
MEDIUM TEPE: Indepy disk
MEDIUM TEPE: Indepy disk
COMPUTER HEADABLE FORM:
MEDIUM SYSTEM: PLOSON, SALE
COMPUTER TERESTAND MANAGEMENT (P.108, Version #1.30
COMPUTER TERESTAND MANAGEMENT (P.108, Version #1.30
CAMPASITORIAN MANAGEMENT (P.108, Version #1.30
REGISTRATION MANAGEMENT (P.108, Version #1.30
MANAGEMENT (P.108, Version WARNER)
MANAGEM
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Sale Landby M.

Pro Marin

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.3%; Score 67; DB 2; Length 432; Best Local Similarity 28.6%; Pred. No. 2.6; Matches 16; Conservative 11; Mismatches 29; Indels
                                                                                                                                                                                                                          ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: PATENTY
COMPUTER: PATENTY
COMPUTER: PATENTY
COMPUTER: PATENTY
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/937,466
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                   APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESSED SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chen, Jing
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSE:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CUSA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us/09/172,528
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFRENCE/DOCKET NUMBER: T97-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09172528
Patent No. 5952469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650) 343-4342 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide US-08-937-466-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-172-528-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 OSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFA-----CYEKL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 PPGQYKSVPNCAMKVFTNEGPTAFFKGLVPSFLRLGSWNVIMFVCFEQLKRELS 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLS 61
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.7%; Score 69; DB 5; Length 306; Best Local Similarity 27.8%; Pred. No. 0.92; Matches 15; Conservative 12; Mismatches 27; Indels
                                                                                                                                                                                                                               Cassard, A.M. et al. publication
Genbank - Locus 37607
                                                                                                                                                                                                                                                  CTHER INFORMATION: Genbank - Locus 37607

HUBLICATION INFORMATION:
AUTHORS: Cassard, A.M. et al.
TITLE: Human Uncoupling Protein Gene: Structure,
PCT-US94-09799-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 KKTLSDVIHPGG--NSHIANG-AAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: GH-30002
FILE REFERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DAYE: 1999-06-30
EARLIER APPLICATION NUMBER: 9704551.2
EARLIER APPLICATION NUMBER: 9705614.7
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER APPLICATION NUMBER: 97305305.1
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTER OF WINGOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09142565A Patent No. 6187560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08937466
Sequence 1, Sequence 5, Sequence 6, Sequence 7, Sequence 1, Sequence 1, September 1 INFORMATION:
APPLICANT: Zhang, Ning
                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 306 amino acids TYPE: amino acid
                                                                                                        TOPOLOGY: Linear
ORIGINAL SOURCE:
ORGANISM: Human
CELL TYPE: Brown adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Lee James Beeley
APPLICANT: Kelly Paine
APPLICANT: Robert James
609-275-1010
                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: HOMO SAPIEN
US-09-142-565-2
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-142-565-2
                                                                                                                                                                                                          FEATURE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
                                                                                                   8 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
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             Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,579
             Score 67; DB 3;
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STATE: CALIFORNIA
                                                          11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION
PROGRAMMEN: US/08/937,466
APPLICATION NUMBER: US/08/937,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORREY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 197-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application US/08775009; Patent No. 5935783; GENERAL INFORMATION: APPLICANT: Gong, Weilong APPLICANT: Bnanuel, Beverly S. APPLICANT: Budarf, Marcia L.
                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    ; Sequence 4, Application US/09503579
; Patent No. 6248561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
             Query Match 13.3%;
Best Local Similarity 28.6%;
Matches 16; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94010
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US-08-775-009-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-503-579-4
                                                                                                                                                                                                              RESULT 13
US-09-503-579-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Ning
APPLICANT: Amaral, M. Catherine
APPLICANT: Amaral, M. Catherine
APPLICANT: Chen, Jin-Long
TITLE OF INVENTION: UCP3 Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.3%; Score 67; DB 2
Best Local Similarity 28.6%; Pred. No. 2.6;
Matches 16; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-009
TELECOMNUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPHONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/318,199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,466
08/937,466
                                 ATTOREX AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFRENCE/DOCKET NUMBER: 197-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09318199 Patent No. 6025469 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 amino acids
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                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-172-528-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-09-318-199-4
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz 6
ADDRESSE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/09268347
Patent No. 6335182
Beneral INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
13.0%; Score 65.5; Di
Best Local Similarity 30.6%; Pred. No. 2.6;
Matches 19; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                  ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 32
LENGTH: 1094
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Search completed: August 27, 2002, 03:58:53 Job time: 4895 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 27, 2002, 03:57:42; Search time 80.04 Seconds (without alignments) 112.849 Million cell updates/sec Run on:

US-09-870-113-10

502 1 MQSLQPDPAARYRNVLEALW......GAAGCVATLLHDAAMNPAEG Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues

Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:* Database:

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	Description	hypothetical prote		α	mtRNA splice defec	probable RNA splic	mtRNA splice defec	probable carrier p	probable phosphate	hypothetical prote	hypothetical prote		mitochondrial phos	hypothetical prote	О	hypothetical prote	probable carrier p	mitochon	probable mitochond	probable mitochond	phosphate transpor	adenylate transloc	2-oxoglutarate/mal	hypothetical prote	+	Ca-dependent solut	uncoupling protein	hypothetical prote	hypothetical prote	hypothetical prote
SUMMAKIES	QI	T26089	A86205	T00582	S55179	T39149	S13533	S44092	S60949	B96830	D84613	JQ1459	T49281	T43493	D84798	T20229	S57116	686383	T51393	T18253	T51595	T05350	A36305	T23170	A56650	T47703	T05577	T45934	18	8
	DB	7	7	7	7	~	7	Н	~	7	7	7	~	~	~	7	7	~	7	7	7	7	~	7	7	~	7	7	~	7
	Length	312	781	331	314	303	304	384	307	296	313	436	363	351	348	310	322	311	353	284	288	392	314	296	314	332	313	358	336	366
dР	Query Match	43.1	26.9	25.9	24.7									17.8	17.7	17.4	17.2	16.9	16.6	16.5	16.5	16.3	16.0	15.8	15.8	15.7	15.6	15.6	15.5	15.5
	Score	216.5	135	130	124	118	106	101.5	95	94.5	94.5	93	90	89.5	83	87.5	86.5	82	83.5	83	83	82	80.5	79.5	79.5	79	78.5	8	78	78
	Result No.	1	7	m	4	ស	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

ADP,ATP carrier pr lactate dehydrogen hypothetical prote	formamidopyrimidin formamidopyrimidin proline dehydrogen	proline dehydrogen probable dicarboxy phosphate transpor	hypothetical prote hypothetical prote hypothetical prote	oxoglutarate/malat hypothetical prote phosphate transpor mitochondrial carr
S31935 E69118 S54524	AI2615 H97397 S66279	AE0633 T49628 T05707	G96770 T32897 S67662	S44091 B96811 T01169 T29640
7 7 7	777	000	000	0000
301 325 368	298 325 1320	1320 282 375	367 650 307	290 418 366 330
15.4 15.3	15.2	15.2	14.8 14.8 14.7	14.5 14.5 14.3 14.2
77.5 77 77	76.5	76.5	74.5 74.5 74	73 73 72 71.5
30 31 32		36 37 38	33 40 41	4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

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RESULT 1
T26089
hypotherical protein W02B12.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T26089
R;Swinburne, J.; Alnscough, R.
Submitted to the EMBL Data Library, October 1995
A;Reference number: Z20149
A;Accession: T26089
A;Accession: T26089
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: Bype: DMA
A;Residues: 1-312 < WILA;Cross-references: EMBL:Z66521; PIDN:CAA91399.1; GSPDB:GN00020; CESP:W02B12.9
A;Experimental source: Clone W02B12
C;Genetics:
A;Gene: CESP:W02B12.9
A;Antrons: 18/3; 286/3
A;Introns: 18/3; 221/3; 286/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Length 312; Indels DB 2; Query Match 43.1%; Score 216.5; DB 2; Best Local Similarity 50.0%; Pred. No. 2.2e-16; Matches 47; Conservative 16; Mismatches 28;

5;

1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60 ŏ

45 MQSLCPCPETKCPTPVHSLMSIVKREGWLRPLRGVNAVAAGSMPAHALYFTVYEKMKGYL 104 g

61 SDVIHPGGNSH-IANGAAGCVATLLHDAAMNPAE 93 QΫ

qq

Apochetical protein [imported] - Arabidopsis thaliana hypothetical protein [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86205
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Atthors: Salzberg, T.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo A;Atthors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.

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mtRNA splice defect-suppressing mitochondrial carrier MRS3 - yeast (Saccharomyces cer C; Specias: Saccharomyces cerevisiae of Seccharomyces cerevisiae of Seccharomyces cerevisiae c; Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000 C; Accession: S55179; S01267; S20228; S56915; S71664 R; Katsoulou, C: Tzermia, M.: Alexandraki, D. submitted to the EMBL Data Library, May 1995 A; Description: The complete sequence of a 40.7 kb segment located on the left arm of yeast hypothetical proteins. A; Reference number: S55159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-314 < RAT>
A; Residues: EMBL: X87371; NID:9854542; PID:9854563
B; Schmidt, C.; Soellner, T.; Schweyen, R.J.
Mol. Gen. Genet. 210, 145-152, 1987
A; Title: Nuclear suppression of a mitochondrial RNA splice defect: nucleotide sequenc
A; Reference number: S01267; MUID:88121698
A; Accession: S01267
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A; Molecule type: DNA
A; Molecule type: DNA
A; Rosidues: 1-86, '2', 88-102,'L',104-127,'Y',129-141,'M',143-187,'R',189-314 <SCH>
A; Cross-references: EMBL:X06239; NID:g3990; PIDN:CAA29582.1; PID:g3991
A; Wiesenberger, G.; Link, T.A.; von Ahsen, U.; Waldherr, M.; Schweyen, R.J.
J. Mol. Biol. 217, 23-37, 1991
A; Title: MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new
A; Reference number: S13532; MUID:91108815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: probably involved in splicing of all intron for COB gene; essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X87371; NID:9854542; PIDN:CAA60822.1; PID:9854563 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
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R;Ratsoulou, C.; Tzermia, M.; Tavernarakis, N.; Alexandraki, D.
Yeast 12, 787-797, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAA39830.1; PID:g3994
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A; Accession: S71664
A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-314 < KAF>
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A; Residues: 19-314 «VIES»
A; Residues: 19-314 «VIES»
A; Cross-references: EMBL:X56445; NID:93992; PIDN:CAA39830.1
R; Katsoulou, C.; Tzermia, M.; Alexandraki, D.
Submitted to the Protein Sequence Database, September 1995
A; Reference number: S56912
A; Accession: S56915
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Best Local Similarity 36.77
Matches 29; Conservative
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A; Residues: 1-314 <KAW>
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Probable
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N'Alternate names: hypothetical protein [imported] - Arabidopsis thaliana
N'Alternate names: hypothetical protein T27E13.10
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Accession: T00582: C84705
R'Rountsley, S.D.: Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaulsumited to the EMBL Data Library, May 1998
A; Description: Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence.
A; Reference number: Z14178
A; Accession: T00582
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL, Accession: T00582
A; Status: Lanslated from GB/EMBL, Accession: T00582
A; Status: Lanslated from GB/EMBL, Accession: T00582
A; Status: Lanslated from GB/EMBL, Accounting M. L. A; Shen, M. I; Town, C.D.; Fujli, C.Y.;
A; Experimental source: cultivar Columbia
A; Experimental source: cultivar Columbia
A; Experimental source: white, O; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUD: 20083487
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Cross - reference can dean analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Cross - reference can dean analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Cross - reference can analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Cross - reference can dean analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Cross - reference can analysis of chromosome 2 of the plant Arabidopsis chaliana.
A; Cross - reference can analysis of chromosome 2 of the plant Arabidopsis chaliana.
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: mitochondrion
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                                                                                                          A;Molecule type: DNA
A;Residues: 1-781 <STO>
A;Crosor = references: GB:AE005172; NID:g8954043; PIDN:AAF82217.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 MQALRPCP-LKPVGIREAFRSIIQKEGPSALYRGIWAMGLGAGPAHAVYFSFYEVSKKYL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 781;
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                                                                                                                                                                                                                                                                                                                                                                                                              26.9%; Score 135; DB 2; 38.9%; Pred. No. 6.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                      A; Status: preliminary
                              A; Accession: A86205
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Best Local Simi
Matches 37;
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probable carrier protein c2 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Ocenorhabditis elegans
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-oct-1999
C; Accession: S44092; 724753
R; Runswick, M.J.; Philippides, A.; Lauria, G.; Walker, J.E.
submitted to the EMBL Data Library, November 1993
A; Reference number: S44090
A; Reference number: S44090
A; Status: preliminary
A; Status: preliminary
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A;Introns: 82/1; 113/1; 153/2; 179/2; 259/3; 359/3
A;Introns: 82/1; 113/1; 153/2; 179/2; 259/3; 359/3
A;Introns: 82/1; 113/1; 153/2; 179/2; 259/3; 359/3
E;4-43,141-193/Domain: ADP,ATP carrier protein repeat homology *status atypical <ACP1
E;45-67/Region: serine-rich
F;201-285/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;201-285/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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A;Molecule type: DNA
A;Residues: 1-384 <WIL>
A;Cross-references: EMBL:Z49070; PIDN:CAA88869.1; GSPDB:GN00020; CESP:T09F3.2
A;Experimental source: clone T09F3
C;Genetics:
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A;Residues: 1-384 <RUN>
A;Cross-references: EMBL:X76116; NID:g472899; PIDN:CAA53722.1; PID:g472900
R;Lloyd, C.
submitted to the EMBL Data Library, April 1995
                                                                                                                                                                            Gaps
                                                                                                                      15 VLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIAN 74
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        Pred. No. 0.00041;
2; Mismatches 40;
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        Best Local Similarity 32.5%; Pr.
Matches 25; Conservative 12;
                                                                                                                                                                                                                                                                                                                                                            124 ALSGTIATIAADALMNP 140
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                                                                                                                                                                                                                                                                                  75 GAAGCVATLLHDAAMNP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: Z19932
A; Accession: T24753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP:T09F3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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513533
mtRNA splice defect-suppressing mitochondrial carrier MRS4 - yeast (Saccharomyces cerevi
NiAlternate names: protein YKR052c
C;Specias: Saccharomyces cerevisiae
C;Specias: Saccharomyces cerevisiae
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jul-2000
C;Accession: S1353; S38126
R;Wiesenberger, G: Link, T.A.; von Ahsen, U.; Waldherr, M.; Schweyen, R.J.
J. Mol. Biol. 217, 23-37, 1991
A;Title: MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new memt
A;Reference number: S13532; MUID:91108815
A;Accession: S1353
A;Molecule type: DNA
A;Residues: 1-304 <AJNO
A;Cross-references: EMBL:X56444; NID:93995; PIDN:CAA39828.1; PID:g3996
R;Vissers, S.; Urrestarazu, L.A.; Jauniaux, J.C.
Submitted to the Protein Sequence Database, March 1994
A;Reference number: S38118
                                                                                                                                                                                            probable RNA splicing proteinmitochondial carrier protein - fission yeast (Schizosacchar Species: Schizosaccharomyces pombe C; Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 C; Accession: T39149
                                                                                                                                                                                                                                                                                                                                                Rioliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A; Reference number: 221748
A; Accession: T39149
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Ratus: preliminary; translated from GB/EMBL/DDBJ
A; Rolecule type: DNA
A; Residues: 1-303 <OLI>
A; Cross-references: EMBL:299168; PIDN:CAB16300.1; GSPDB:GN00066; SPDB:SPAC8C9.12c
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology C; Keywords: duplication; mitochondrion; transmembrane protein F;20-109/Domain: ADP, ATP carrier protein repeat homology <ACPT>F;117-201/Domain: ADP, ATP carrier protein repeat homology <ACPT>F;206-301/Domain: ADP, ATP carrier protein repeat homology <ACPZ>F;206-301/Domain: ADP, ATP carrier protein repeat homology <ACPZ>
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A; Molecule type: DNA
A; Residues: 1-304 <VIS>
A; Cross-references: EMBL: 228277; NID: 9486506; PID: 9486507; MIPS: YKR052c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 303;
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Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: SGD:S0001760; MIPS:YKR052c
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132 KTAISGACATTASDALMNP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 NGAAGCVATLLHDAAMNP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SPDB:SPAC8C9.12c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 11R
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18.8%;
ilarity 37.9%;
Conservative
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Best Local Similarity
Matches 27; Conserva
                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                  206 AGGLAG 211
                                                                                                                                                                                                                                                                                                      73 ANGAAG 78
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                                                        Query Match
Best Local Simi
Matches 25;
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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Razo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.Reference number: A86141; MuID:21016719

A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 30, 'x', 32, 'I', 34-39 <GUE>
R; Galisson, F: Dujon, B.
Yeast 12, 877-885, 1996
A; Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV
A; Reference number: S71713; MUID:96437977
               A;Cross-references: EMBL:X92441; NID:g1050762; PID:g1050774
R;Boyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Michaux, G.; Thierry, A.; Dujon, submitted to the Protein Sequence Database, July 1996
A;Reference number: S67104
                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-307 < ABN >
A; Experimental source: EMBL: 275130; NID: 91420513; PID: 91420514; MIPS: YOR222w
A; Experimental source: strain S288C
B; Guerin, B.; Bukusoglu, C.; Rakotomanana, F.; Wohlrab, H.
J; Biol. Chem. 265, 19736-19741, 1990
A; Title: Mitochondrial phosphate transport. N'ethylmaleimide insensitivity correlates vA; Reference number: A37984; MUID: 91060585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Superfamily: ADP,ATP carrier protein repeat homology cACP-5;9-107/Domain: ADP,ATP carrier protein repeat homology cACP-5;15-201/Domain: ADP,ATP carrier protein repeat homology cACP2-5;208-300/Domain: ADP,ATP carrier protein repeat homology cACP2>
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A;Cross-references: GB:AE005173; NID:96453859; PIDN:AAF09043.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-307 <GAW>
A; Residues: 1-307 <GAW>
A; Cross-references: EMBL:X92441; NID:g1050762; PIDN:CAA63185.1; PID:g1050774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F19K16.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 HIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 23; Conserv
A; Residues: 1-307 <GAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: B37984
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Bil protein precursor - maize
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Date: 17-aug-1992 #text_change 24-Sep-1999
C;Accession: JQ1459
R;Sullivan, T.D.; Strelow, L.I.; Illingworth, C.A.; Phillips, R.L.; Nelson Jr., O.E. Plant Cell 3, 1337-1346, 1991
A;Title: Analysis of maize brittle-1 alleles and a defective suppressor-mutator-induc A;Reference number: JQ1459; MUID:93005685
A;Accession: JQ1459
A;Molecule type: mRNA
A;Residues: 1-436 <SUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein At2g22500 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: D84613
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter A721, Tell-10 Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: D84613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-313 <STO>
A;Cross-references: GB:AE002093; NID:g4544443; PIDN:AAD22351.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 ILRRQGLQGLYRGLTITVLRDAPAHGLYFWTYEYVRERL----HPGCRKTGQENLRTMLV 205
                                                                                                                                                           22 IIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPG----GNSH----I 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD--VIHPGGN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M79333; NID:q168425; PIDN:AAA33438.1; PID:q168426 C;Comment: This protein acts as an adenylate translocator in amyloplasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 206/3; 260/3
C;Superfamily: Btl protein; ADP,ATP carrier protein repeat homology
C;Keywords: chloroplast, duplication; transmembrane protein
E;1-75-Domain: transit peptide (amyloplast) #status predicted <TNP>
F;76-436/Product: Btl protein #status predicted <MAT>
F;131-217/Domain: ADP,ATP carrier protein repeat homology <ACPl>
                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 313;
Score 94.5; DB 2; Length 2
Pred. No. 0.0077;
8; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.8%; Score 94.5; DB 2; Length 3 ilarity 31.8%; Pred. No. 0.0081; Conservative 23; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 THVSASFAAGFVASV----ASNPVD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 SHI-ANGAAGCVATLLHDAAMNPAE 93
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probable mitochondrial carrier protein [imported] - Arabidopsis thaliana probable mitochondrial carrier protein [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: D84798
R;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M; Koo, H; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Recence number: A84420; MUID:20083487
A;Recession: D84798
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <STO>
A;Cross-references: GB:AE002093; NID:94895195; PIDN:AAD32782.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 5
A;Introns: 14/1; 63/1; 155/2; 256/2; 299/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA99811.1; GSPDB:GN00023; CESP:C54G10.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pypothetical protein C54G10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T20229
R;Matthews, L.
R;Matthews, L.
A;Reference number: 219240
A;Reference number: 219240
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-310 <WILD>A;Cross-references: EMBL: 275532; PIDN: CAA99811.1; GSPDB: GN00023; CESP: C54G10
C;Genetics: Control of the control of
                                                                                                                                                                        92 DP-TRFTGTMDAFVKIVRHEGTRTLW---SGLPATLVMTVPATAIYFTAYDQLKAFLCGR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                           7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTL-
                                       21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.7%; Score 89; DB 2; Length 348; Best Local Similarity 31.5%; Pred. No. 0.037; Matches 28; Conservative 13; Mismatches 34; Indels
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLK--
   Similarity 32.3%; Pred. No. 0.033; 31; Conservative 12; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 87.5; DB 2;
Pred. No. 0.048;
                                                                                                                                                                                                                                                                                          148 ALTSDLYAP------MVAGALARLGTVTVISPLE 175
                                                                                                                                                                                                                                               61 ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 DLV----VSLVSGGLAGAVSSTDDKLFDA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 DVIHPGGNSHIANGAAGCVATL---LHDA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.48;
29.38;
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Best Local Similarity
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          Local
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       Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitochondrial phosphate transporter - Arabidopsis thaliana
Millernate names: protein T21J18.120
G:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-12000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
G:Accession: T49281
R:Riseger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, Submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25021
A:Reference number: Z25021
A:Reference resion: T49281
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-363 <RIE>
A;Cross-references: EMBL:AL132963; GSPDB:GN00061; ATSP:T21J18.120
A:Experimental source: cultivar Columbia; BAC clone T21J18
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Reywords: mitochondrion
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C;Species: Homo sapiens (man)
C;Date: 21-Jan.2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T43493
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A;Reference number: 222516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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0
                                                                                                                                                                                                                                                                                                                                                                                       Length 351;
F;226-312/Domain: ADP,ATP carrier protein repeat homology <ACP2> F;223-47/Yomain: transmembrane #status predicted <TM1> F;323-413/Domain: ADP,ATP carrier protein repeat homology <ACP3> F;327-347/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                               , DB 2; Le.,
                                                                                                                                                                                                               Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                        ; Score 93; DB 2
; Pred. No. 0.017
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.9%; Score 90; DB Best Local Similarity 28.9%; Pred. No. 0.03 Matches 28; Conservative 18; Mismatches
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                                                                                                                                                                                                           18.5%;
41.2%;
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Best Local Similarity
Matches 21; Conser
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-351 <AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: ATSP: T21J18.120
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A; Note: DKFZp434C119.1
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Matches 27; Conservative 14; Mismatches 36; Indels 15; Gaps
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Search completed: August 27, 2002, 03:57:43 Job time: 4949 sec

us-09-870-113-10.rsp

Page 1

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GenCore version 4.5
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OM protein - protein search, using sw model

August 27, 2002, 04:16:48; Search time 37.5 Seconds (without alignments) 97.057 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-870-113-10 502 1 MQSLQPDPAARYRNVLEALW.....GAAGCVATLLHDAAMNPAEG

94

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	0566 sacc	P23500 saccharomyc	Q99297 saccharomyc	P29518 zea mays (m			P33303 saccharomyc	P22292 bos taurus	Q02978 homo sapien		Q27238 anopheles g	-	Q03829 saccharomyc	P10503 salmonella	Q9h1k4 homo sapien		P97700 rattus norv	Q9h2d1 homo sapien	P56499 rattus norv	Q9va73 drosophila	O9qzd8 mus musculu	-		Q59752 rhizobium m		Q10442 schizosacch	P55916 homo sapien	Q09461 caenorhabdi	097649 sus scrofa	0	_	6	Q9bqt8 homo sapien
SUMMARIES		qi	MRS3_YEAST	MRS4_YEAST	ODC2_YEAST	BT1_MAIZE	CG69_HUMAN	DNC_HUMAN	SFC1_YEAST	M2OM_BOVIN	M2OM_HUMAN	YG5F_YEAST	ADT_ANOGA	M2OM_MOUSE	YM39_YEAST	PUTA_SALTY	SA18_HUMAN	DIC_HUMAN	M2OM_RAT	MFT_HUMAN	UCP3_RAT	CMC1_DROME	DIC_MOUSE	ADT_CHLRE	PUTA_KLEAE	FPG_RHIME	UCP1_HUMAN	YDE9_SCHPO	UCP3_HUMAN	YQ51_CAEEL	UCP3_PIG	ADT1_YEAST	ADT1_ARATH	UCP3_CANFA	ODC_HUMAN
		ngth DB	314 1																				287 1								308 1		381 1		299 1
đ	Query	Match Length	24.7	21.1	•	œ,	۲.	۲.	17.2	Ġ.	'n	15.5	ů.	15.4	5.3	5.2	∞.	۰		.2	۲.	٦.	0	σ.	æ.	٠.	.7	.7	9.	9.	13.5	13.5		13.4	13.3
		Score	124	106	95	93	89.5	88	86.5	80.5	79.5	78	77.5	77.5	11	76.5	74.5	73.5	73.5	71.5	71		70.5		69.5	69	69	69	68.5	68.5	89	89	68	67.5	29
	Result	No.	+	7	m	4	S	ø	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

P56501 mus musculu P39953 saccharomyc	P40556 saccharomyc Q00319 candida boi Q12375 saccharomyc		P05141 homo sapien P32007 bos taurus	P79110 bos taurus Q41629 triticum ae	Q41630 triticum ae
UCP3_MOUSE YEA6_YEAST	YIA6_YEAST P47B_CANBO ORT1_YEAST	CMC3_CAEEL CMC2_CAEEL	ADT2_HUMAN ADT3_BOVIN	TXTP_BOVIN ADT1_WHEAT	ADT2_WHEAT
чĻ		п п			-
308	373 419 292	587 588	298 298	311 331	331
13.3	13.3 13.3	13.2 13.2	13.1 13.1	13.1	13.1
67	67 67 66.5	66.5 66.5	99 99	99 99	99
34 35	36 37 38	39 40	41	44	45

ALIGNMENTS

MRS3_Y	RESULT I MRS3_YEAST									
ΙD	MRS3_YEAST	STANDARD;	; o	PRT;	314	AA.				
AC		,								
i i	01-JUL-1989 (Re	11.	Created)	_	1					
<u> </u>		(Kel. 32, 1	Last se	sedneuce nbdare)	nbaa	ce)				
5 2	12-DEC-1998 (Re	(Rel. 3/, Last	Last an	annotation update)	dn u	date)				
Э ;	Mitochondrial KNA	ANA SPIIO	Б	protein MRS3.	K53.					
2 0	MKS3 OK IJLI33W OK JU6/5.	V OK JUB	/5.		1					
SO	Saccharomyces cerevisiae (Baker's yeast).	erevisi	зе (вак	er's ye	ast)					
38	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch	Ji; ASCO	nycota;	Saccha	romy	cotina	; sacchai	saccharomycetes;	es;	
3 8	saccharomycera.	les; sac	charomy	ceracea	υ 	accnar	omyces.			
X S	NCBI_TaxID=4932;	.;								
Z C	[T]	6								
א ק ה	SECOENCE FROM N.A.									
X	JIMIN-100/NIC1, MEDI.TNE=88121698: DubMed=2448588:	A DuhMe	-d=2448	58.8						
R P	Schmidt C., Soe	allner T	Schw	even R.						
RT	"Nuclear suppre	suppression of a	f a mit	a mitochondrial RNA	ial 1		splice defect: nucleotide	ect: nuc	cleotide	
RT	sequence and d	and disruption of the MRS3 gene.";	n of th	e MRS3	gene					
RL	. Gen.	. 210:14	45-152(1987).						
RN	[2]									
RP	REVISIONS, SEOU	SEQUENCE FROM N.A.	OM N.A.							
L C	STRAIN-M1301;	1								
ž i	MEDLINE=91108815; PubMed=1/03236;	Lo; PubMe	ed=1703	236;	;		;			
¥ 5	Wiesenberger G	, yntd ,	r.A., v	on Anse		, Wald	G., Link T.A., von Ansen U., Waldherr M., Schweyen K.J	schweye	Schweyen R.J.;	
1 1	MKS3 and MKS4	two su	ossardo	ES OF III	CKNA	Spire	rud derec	irs in	yeast,	
K.	are new members	or the	mitoch	ondrial	Car	rier i	tamıly.";			
1 E	U. MOI. BIOI. ZI/:Z3-3/(I991). [3]	617:23-3.	(1661)							
00	SECTIENCE FROM N A	4								
2	STRAIN=5288C / FY1679:	FY1679								
2 X	MEDLINE=96408771; PubMed=8813765;	1; PubMe	ed=8813	765;						
RA	Katsoulou C., ?	zermia	M., Tav	ernarak	is N	., Ale	xandraki	D.;		
RŢ	"Sequence analysis of a 40.7 kb segment	sis of	40.7	kb segm	ent	from t	from the left arm of		yeast	
RT	chromosome X re	veals 1	4 known	known genes and 13	and	13	new open reading		frames	
RI	including homologues of	co senso	f genes	cluste	red	on the	right a	in of		
	Chromosome XI.	19061								
1 5	- 1 - FITNCT TON . N	RS3 SUP	PRESERS	A MTTO	INOH	PETAL.	SPLICE DE	FECT TI	AHE N	
, 2	FIRST INTRO	N OF THE	E COB G	ENE. IT	MAY	ACT A	S A CARRI	ER, EXI	ERTING	
ပ္ပ	ITS SUPPRESSOR ACTIVITY VIA MODULATION OF SOLUTE CONCENTRATIONS	SSOR ACT	IVITY V.	IA MODU	LATIC	ON OF	SOLUTE CC	NCENTR		NH
ည	THE MITOCHONDRION (POSSIBLY OF CATIONS).	ONDRION	(POSSIB	LY OF C.	ATIO	NS).				
ဗ	-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial	LOCATIC	ON: Int	egral m	embra	ane pr	otein. Mi	tochon	drial	
ပ္ပ		ane.								
ပ္ပ	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.	BELONG	S TO TH	MITOC	HONDI	RIAL C	ARRIER F?		STRONG,	
ပ္ပ	TO YEAST ME	S4; BOTI	H PROTE	INS MAY	BE	SOFOR	YEAST MRS4; BOTH PROTEINS MAY BE ISOFORMS OF THE SAME		CARRIER	
3 8	PROTEIN.			1		1		1		
3 5	This SWISS-PROT entry is	Potro	S CODY	s convright	1	prod	convright. It is produced through a collaboratio	nah a c	hrongh a collaborat	at 1
000	between the Sv	riss Inst	itute (of Bioi	forn	natics	and the	EMBL	outstat	ton
ပ္ပ	the European Bioinformatics Institute. There are no restrictions on it	oinform	atics In	stitute		There	are no 1	estrict	tions on	
ပ္ပ	use by non-profit institutions as long	ofit ir	stitut	ions as	long	y as	its conte	ent is	in no	3
ខ្ល	modified and the	nis state	ement i	s not r	emove.	ed. U	sage by	and fo	or comme	rci
ပ္ပန	entities requires a license agreement (See http://www.isb-sib.ch/announce	es a lic	cense a	greemen	t (Se	e htt	D://www.i	sp-sip.	.ch/anno	nuc
ر	or sello all ella	וו הס דונ	ממפד	SD-STD.	. (11)					

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ODC2_YEAST
Q99297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walker J.E.
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SEQUENCE
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REPEAT
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ODC2_YEAST
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-!- FUNCTION: MRS4 SUPPRESES A MITCHONDRIAL SPLICE DEFECT IN THE FIRST INTRON OF THE COB GENE. IT MAY ACT AS A CARRIER, EXERTING ITS SUPPRESESOR ACTIVITY VIA MODULATION OF SOLUTE CONCENTRATIONS IN THE MITCHONDRION (POSSIBLY OF CATIONS). NOT ESSENTIAL.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wiesenberger G., Link T.A., von Ahsen U., Waldherr M., Schweyen R.J.; "MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new members of the mitochondrial carrier family.";
                                                                                                                                                                                                                                                                                                                                                       72 KNMLSQISHISTSEGTLALWKGVQSVILGAGPAHAVYFGTYEFCKKNLIDSSDTQTHHPF 131
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                  13 RNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHI 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. STRONG, TO YEAST MRS3; BOTH PROTEINS MAY BE ISOFORMS OF THE SAME CARRIER
                                       EMBL; X87371; CAA608221; --
EMBL; Z49408; CAA89428.1; --
EMBL; Z49408; CAA89428.1; --
EMBL; S20208; S20208
SCD; S0003669; MRS3.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRS4 OR YKR052C.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                      Score 124; DB 1; Length 314; Pred. No. 7.4e-07;
                                                                                                                                                                                                                                                                                                            41; Indels
                                                                                                                                                                                                                                                        861145CE6E4EF321 CRC64;
                                                                                                                                                      BLOCK I (APPROXIMATE).
BLOCK II (APPROXIMATE).
BLOCK III (APPROXIMATE).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                 II (APPROXIMATE).
III (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                            MRS4_YEAST

ID MRS4_XEAST
AC P23500.

DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Mitochondrial RNA splicing protein MSR4.
                                                                                                                                                                                                                                                                                                  Pred. No. 7.4e-
9; Mismatches
                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                              POTENTIAL
                    X56445; CAA39830.1; ALT_INIT.
X06239; CAA29582.1; ALT_SEQ.
X87371; CAA60822.1; -T_SEQ.
Z49408; CAA89428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-M1301;
MEDLINE-91108815; PubMed-1703236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Biol. 217:23-37(1991).
                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                      Query Match 24.7%;
Best Local Similarity 36.7%;
Matches 29; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                         73 ANGAAGCVATLLHDAAMNP 91
                                                                                                                                                                                                                                                       34501
            X56445; CAA39829.1;
                                                                                                                                                                                                                                                       314 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                            mRNA processing.
REPEAT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 MISQISKISTWEGSMALWKGVQSVILGAGPAHAVYFGTYEFCKARLISPEDMQTHQPMKT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 VLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIAN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Palmieri L., Agrimi G., Runswick M.J., Fearnley I.M., Palmieri F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galisson F., Dujon B.; "Sequence and analysis of a 33 kb fragment from the right arm of "Sequence and analysis of a saccharomyces cerevisiae."; chromosome XV of the yeast Saccharomyces cerevisiae."; reast 12:877-885(1996).
                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; mRNA processing: 110 BIOCK I (ADDDANTMART)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.1%; Score 106; DB 1; Length 304; 32.5%; Pred. No. 8.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5ABBF9858B547EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOCK I (APPROXIMATE).
BLOCK II (APPROXIMATE).
BLOCK III (APPROXIMATE)
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial 2-oxodicarboxylate carrier 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                               EMBL; X56444; CAA39828.1; -.
EMBL; 228277; CAA82130.1; -.
PIR; S1333; S13533.
SGD; S0001760; MRS4.
InterPro; IPR001993; Mitoch_carrier.
Pram; PFO0153; MICC_CARR: 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
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STRAIN=S288C / FY1679;
MEDLINE-96437977; PubMed=8840505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MM;
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124 ALSGTIATIAADALMNP 140
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33307 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Conservative
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202
304
41
102
1139
1194
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Best Local Similarity
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POTENTIAL.
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                                                                                                                                                                                                                                                                                              46627 MW;
                                                                                                                            EMBL; M79333; AAA33438.1; -.
                                                                                                                                                                                                                                                                                                                                                            21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                        436
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                                                                                                                                          JQ1459; JQ1459.
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229 2
327 3
436 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG69_HUMAN
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CG69_HUMAN
                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oxoglutarate, adipate, glutarate, 2-oxopimelate, oxaloacetate, cirrate and malate. The main physiological role is probably to supply 2-oxoadipate and 2-oxoglutarate from the mitochondrial matrix to the cytosol where they are used in the biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 RYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNS 70
                                                            lysine and glutamate, respectively, and in lysine catabolism. SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suppressor-mutator-induced mutable aliele.";
Plant Cell 3:137-1348(1991).
-!- FUNCTION: COULD PLAY A ROLE IN AMYLOPLAST MEMBRANE TRANSPORT.
-!- SUBCELLULAR LOCATUON: CHOICOPLAST; amyloplast.
-!- TISSUE SPECIFICITY: ENDOSPERM OF DEVELOPING KERNELS.
                                                                                                                                                                                                                                                                                                                                                Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
 membranes of mitochondria. Can transport 2-oxoadipate, 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sullivan T.D., Strelow L.I., Illingworth C.A., Phillips R.L., Nelson O.E. Jr.;
                                                                                                DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.9%; Score 95; DB 1; Length 307; 27.7%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
4089082A64DBA97C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Analysis of maize brittle-1 alleles and a defective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brittle-1 protein, chloroplast precursor.
                                                                                                                                                                                                                                                                                                                                              Mitochondrion; Inner membrane; Repeat; TRANSMEM 10 30 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                  SGD; S0005748; ODC2.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                       Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93005685; PubMed=1668652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 HIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
                                                                                                                                                                                                                                                                                                                                                                                                             34007 MW;
                                                                                                                                                                                                                                         EMBL; 275130; CAA99440.1; -. EMBL; X92441; CAA63185.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                        122 1
215 2
280 3
307 AA;
                                                                                       inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BT1_MAI2E
P29518:
                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BT1_MAIZE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Overexpression of the human 2-oxoglutarate carrier lowers mitochondrial membrane potential in HBK-293 cells: contrast with the unique cold-induced mitochondrial carrier CGI-69."; Biochem. J. 353:369-375(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu X.X., Lewin D.A., Zhong A., Brush J., Schow P.W., Sherwood S.W., Pan G., Adams S.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=20272150; Pubmed=10810093;

Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;

Lai C.-H., Chou G. ovel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";

Genome Res. 10:703-713(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND
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-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002067; Mit_carrier.
InterPro; IPR001093; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSTTE; PS00215; MITOCH_CARRIER; 1.
Transit peptide; Chloroplast; Amylophast; Transmembrane.
TRANSIT 1 75 CHLOROPLAST (POTENTAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9600C05F603E9DAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial carrier protein CGI-69 (PRO2163).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRITTLE-1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.5%; Score 93; DB 1;
41.2%; Pred. No. 0.0038;
Live 7; Mismatches 23
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                                                               [4]
SEQUENCE FROM N.A. (ISOFORM 1).
Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human CDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                         "Functional prediction of the coding sequences of 79 new genes deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1/CGI-69L (shown here) and 2, are produced by alternative splicing.
-!- TISSUE SPECIFICITY: Expressed in many tissues. Abundant in testis
                                                                                                                                                                                                                                                                                                           Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                    by analysis of cDNA clones from human fetal liver.", Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
Wambutt R., Korn B., Klein M., Poustka A.; "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
LPSSLQSTG -> W (IN ISOFORM 2).
                                                                                                                                                                                                                               Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> R (IN REF. 6).
952AA3DB5F5F9BD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      -! - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_012756
                                                                                                                                                                                                                                                                         SEQUENCE OF 15-359 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC001398; AAH01398.1; -.
EMBL; BC009330; AAH09330.1; -.
EMBL; AF119864; AAF69618.1; -.
InterPro; IPR001993; Mitcoh_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٠
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                                                                                                                                                                                            (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF317711; AAG60687.1; -.
EMBL; AF151827; AAD34064.1; -.
EMBL; AL133584; CAB63728.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AK026060; BAB15341.1; -. BC001398; AAH01398.1; -.
                                 analysis of 500 novel complete
Genome Res. 11:422-435(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39214 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00153; mito_carr;
                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOF)
TISSUE-Brain, and Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                        inner membrane.
                                                                                                                                                                                                                                                                                             liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266
                                                                                                                                                                                                                                                                                            rissue-Fetal
                                                                                                                                                                                                                            Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

DISEASE: Likely to be medically important by providing the means
of uptake into mitochondria of nucleoside analogs, leading to the
mitochondrial impairment that underlies the toxic side effects of
such drugs in the treatment of viral illnesses, including AIDS,
100 DP-TRETGTMDAFVKIVRHEGTRTLW---SGLPATLVMTVPATAIYFTAYDQLKAFLLGR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dolce V., Fiermonte G., Runswick M.J., Palmieri F., Walker J.E.; "The human mitochondrial deoxynucleotide carrier and its role in the toxicity of nucleoside antivirals."; Paroc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Expressed in all tissues examined except for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           placenta. Highest levels in colon, kidney, lung, testis, spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                          01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and in cancer therapy. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Renard S., Mondesert G., Besnard F.;
"MUP 1, a mitochondrial uncoupling protein.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                      156 ALTSDLYAP-----MVAGALARLGTVTVISPLE 183
                                                     93
                                                                                                                                                                              ¥
                                                     ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ251857; CAC27560.1; -. EMBL; AJ301616; CAC37793.1; -. EMBL; AF182404, AAG16903.1; -. EMBL; BC001075; AAH01075.1; -. EMBL; BC005120; AAH05120.1; -.
                                                                                                                                                                                                                                                                                     protein 1).
SLC25A19 OR DNC OR MUP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitochondrial DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inner membrane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11226231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Lung;
                                                                                                                                                                              DNC_HUMAN
                                                       61
                                                                                                                                                            DNC_HUMAN
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Gaps

21;

17.8%; Score 89.5; DB 1; Length 359; 32.3%; Pred. No. 0.0077; ive 12; Mismatches 32; Indels 2

Conservative

Similarity

Query Match Best Local Simi Matches 31;

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DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTL--- 60

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Palmieri F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M2OM BOVIN
                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
M2OM_BOVIN
                                                                                                                                                                                       SGD;
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                                                                                                                                                                                                                                                                                                                      4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial. INDUCTION: BY ETHANOL OR ACETATE AS SOLE CARBON SOURCES. REPRESSED BY GLUCOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Succinate/fumarate mitochondrial transporter (Regulator of acetyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                54 DPSAKYHGILQASRQILQEGPTAFWKGHVPAQILSIGYGAVQFLSF-----EMLTEL 106
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                     7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE-94203187; PubMed-7908717; Fernandez E., Rodicio R.; "ACRI, a gene encoding a protein related to mitochondrial carriers, is essential for acetyl-CoA synthetase activity in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Palmieri L., Lasorsa F.M., De Palma A., Palmieri F., Runswick M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetase activity).
SFC1 OR ACR1 OR YJR095W OR J1921.
Sacoharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Sa
                                                                                                             Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                 Length 320;
                                                                                                                                                                                                                                                            Score 89; DB 1; Lengtn ....
Pred. No. 0.0077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Ramezani Rad M., Kirchrath L., Hollenberg C.P.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                        57CE0F01D538B1BE CRC64;
                                                                                                                                                                                                                                                              17.7%; Scor.
27.3%; Pred. No. v...
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 AA
         InterPro; IRR01993; Mitoch_carrier.
InterPro; IRR01903; Mit_carrier.
InterPro; IPR002067; Mit_carrier.
Prinrs; PR00926; MITOCARRIER.
PROSITE: PS00215; MITOCH CARRIER; 1.
Mitochondrion; Inner membrane; Repeat; 7
TRANSMEM 19
                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 IHPGG-----NSH-IANGAAGCVATL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Gen. Genet. 242:727-735(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98055465; PubMed-9395087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 28, Created)
                                                                                                                                                                                                                        35511 MW;
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                122
173
173
329
320 AA;
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION.
MIM; 606521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994
                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFC1_YEAST
P33303;
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                                                                                                                                                                                 TRANSMEM
TRANSMEM
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Best Local (
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VREHLENLGIFKKNDTPKPKPLK -> RKGAFQKIWVYSRR
matics Institute. There are no restrictions on institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structural relationship to other mitochondrial transport proteins.";
Biochemistry 29:11033-11040(1990).
-!- FUNCTION: CATALYZES THE TRANSPORT OF 2-OXOGLUTARATE ACROSS THE
INNER MITOCHONDRIAL MEMBRANE IN AN ELECTRONEUTRAL EXCHANGE FOR MALATE OR OTHER DICARBOXYLIC ACIDS, AND PLAYS AN IMPORTANT ROLE
IN SEVERAL METABOLIC PROCESSES, INCLUDING THE MALATE-ASPARTATE
SHUTTLE, THE OXOGLUTARATE/ISOCITRATE SHUTTLE, IN GLUCONEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIC25All OR SIC20A4.

Bos taurus (Bovine).

Eukaryota; Metazooa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 QPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLS---
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"Sequences of the human and bovine genes for the mitochondrial 2-
oxoglutarate carrier.";
DNA Seq. 3:79-88(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Sequence of the bovine 2-oxoglutarate/malate carrier protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Mitochondrial 2-oxoglutarate/malate carrier protein (OGCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTHQSQSH (IN REF. 1).
EC29718A0F5011A7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.2%; Score 86.5; DB 1; Sest Local Similarity 29.6%; Pred. No. 0.015; Matches 24; Conservative 14; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- TISSUE SPECIFICITY: HEART, LIVER, AND BRAIN.
-!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM LACTATE, AND IN NITROGEN METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001993; Mitoch_carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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MEDLINE=93091249; Pubmed-1457818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Heart;
MEDLINE=91105033; PubMed=2271695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Transport; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 QMDVLPSWETSCIGLISGAIG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 -- DVIHPGGNSHIA--NGAAG 78
                                                                                                                                                                                        EMBL; Z25485; CAA80973.1; -. EMBL; Z49595; CAA89624.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                           SFC1
                                                                                                                                                                                                                                                           PIR; S36407; S36407
PIR; S43280; S43280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 AA;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                        REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           LQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YU W., Glbbs R.A.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE TRANSPORT OF 2-0XOGLUTARATE ACROSS THE
INNER MITOCHONDRIAL MEMBRANE IN AN ELECTRONEUTRAL EXCHANGE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=93091249; PubMed=1457818;
Iacobazzi V., Palmieri F., Runswick M.J., Walker J.E.;
"Sequences of the human and bovine genes for the mitochondrial 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                            Inner membrane; Repeat; Transmembrane; Transport.
PTM: The N-terminus is blocked. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                Query Match
16.0%; Score 80.5; DB 1; Length 313;
Best Local Similarity 30.0%; Pred. No. 0.071;
Matches 27; Conservative 15; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MZOM_HUMAN STANDARD; PRT; 313 AA.
002978; 075537;
01-JUL-1993 (Rel. 26, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
Mitochondrial 2-cxoglutarate/malate carrier protein (OGCP)
SLC25A11 OR SLC20A4.
                                                                                                                                                                                                                                                                                                                                 2610CF23193DD419 CRC64;
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POTENTIAL.
POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 IHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                         InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                 34040 MW;
                                                                                                                    EMBL; X66115; CAA46906.1; -.
EMBL; M58703; AAA30671.1; -.
EMBL; M60662; AAA30672.1; -.
                                                                                                                                                                                                                                 41
100
139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutarate carrier.";
Seq. 3:79-88(1992).
                                                                                                                                                                                                                                                                 201
                                                                                                                                                     PIR; A36305; A36305.
PIR; S29597; S29597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                      209
313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                 108
                                                                                                                                                                                                          Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
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TRANSMEM
                                                                                                                                                                                                                                                                                       FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome VII reveals the presence of three new open reading frames
                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%; Score 79.5; DB 1; Length 313; 31.1%; Pred. No. 0.092; tive 12; Mismatches 49; Indels
                                                                                                                                                                                        SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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Mazzoni C., Ruzzi M., Rinaldi T., Solinas F., Montebove F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of a 10.5 kb DNA fragment from the yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> M (IN REF. 1).
A4831A2E1A9F175A CRC64;
                                                                                                                                                               DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 AA.
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01-077-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion; Inner membrane; Repeat; Trai
INIT_MET 0 0 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Last annotation up
Putative mitochondrial carrier YGR257C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 GYFSDNI-LCHFCASMISGLVTTAASMPVD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro, IPR001993; Mitoch_carrier. Pfam; Pf00153; mito_carr; 3. PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF070548; AAC28637.1; -. PIR; S29598; S29598.
MIM; 604165; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X66114; CAA46905.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                         inner membrane
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209
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118
182
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280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YG5F_YEAST
P53320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Arakawa T., Hara A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Arakawa T., Hara A., Shibata K., Kono H., Adachi J., Fukuda S.,
RA Arakawa T., Rawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori P., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsudo Y., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Machara I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Hilming L.,
M. Haysahlzani Y., Rawai Y., Kawaii H., Kohtsuki S.,
M. Haysahlzani Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                 Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                            15.4%; Score 77.5; DB 1; Length 301; 28.2%; Pred. No. 0.15;
tive 13; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrial 2-oxoglutarate/malate carrier protein (OGCP). SLC25All.
                                                                                                                                                                                                                                                                                                                          4CC9E17C9F8DA08B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 AA.
                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                        EMBL; L11618; AAB04104.1; -.
EMBL; L11617, AAB04105.1;
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                           Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Tongue;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                   31 1
93 2
136 3
197 4
233 5
293 6
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 28.28
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 FVSWAIAQVVT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 IANGAAGCVAT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                   Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M20M_MOUSE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute of Three are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
                  Yeast 13:369-372(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;
"A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles
gambiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
0
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-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                   Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 1.
Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                       -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 78; DB 1; Length 366;
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: ||| :| || :| || :: || || :| || 101 KFNGTLEAFTKIASVEGITSLWRGISLTLLMAIPANMVYFSGYEYIR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 RYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B0358B6EE818CB1E CRC64;
                                                  inner membrane (Potential).
-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                     SGD; S0003489; rGR257C.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94348635; PubMed-8069414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40763 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.5%;
                                                                                                                                                                                                                                                                EMBL; X99228; CAA67613.1; -. EMBL; Z73042; CAA97286.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
   of a tRNAThr gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              124
162
168
268
366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translocator) (ANT).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7165;
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01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADT_ANOGA
Q27238;
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TRANSMEM
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1;

Gaps

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us-09-870-113-10.rsp

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Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
             Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: CATALYZES THE TRANSPORT OF 2-OXGLUTARATE ACROSS THE INNER MITOCHONDRIAL MEMBRANE IN AN ELECTRONEUTRAL EXCHANGE FOR MALATE OR OTHER DICARROXILIC ACIDS, AND PLAXS AN IMPORTANT ROLE IN SEVERAL METABOLIC PROCESSES, INCLUDING THE MALATE-ASPARTATE SHUTTLE, THE OXOGLUTARATE/ISOCITRATE SHUTTLE, IN GLUCODOGENESIS FROM LACTATE, AND IN NITROGEN METABOLISM (By similarity).

-!-SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).

-!-DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

-!-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 LPADQRRGYKNVFNALVRIAREEGVPTLWRGCIPTMARAVVVNAAQLASYSQSKQFLLDS 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.4%; Score 77.5; DB 1; Length 313; 31.1%; Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hunt S., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22FB47E21B39A353 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Putative mitochondrial carrier YMR166C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 IHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK009824; BAB26524.1; -.
EMBL; AK009487; BAB26319.1; -.
EMBL; BC003455; AAH03455.1; -.
MGD; MGI:1915113; Slc25a11.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00153; mito_carr; 3.
PE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34023 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
100
139
239
239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108
209
313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
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Q03829;
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TRANSMEM
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Matches
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MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|||::| | ||:| :| :| :| ||:| :| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
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SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Bifunctional puth protein [Includes: Proline dehydrogenase (BC 1.5.99.8) (Proline oxidase); Delta-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93241961; PubMed=8479928; Allen S.W., Senti-Willis A.E., Maloy S.R.; DNA sequence of the putA gene from Salmonella typhimurium: a bifunctional membrane—associated dehydrogenase that binds DNA."; Nucleic Acids Res. 21:1676-1676(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z49705; CAA89802.1; -. SGD; S0004776; YMR166C. InterPro; IPR001993; Mitoch_carrier. PF00153; mito_carr; 3. Pfam; PF00153; mito_carr; 3. PROSITE; PS00215; MITOCH_CARRIER; 2. Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
                                                              inner membrane (Potential).
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 77; DB 1; Length 368;
; Pred. No. 0.21;
16; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B583100018DF045D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1320 AA
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nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 I----THLSAGFLG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 IHPGGNSHIANGAAG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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152
260
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315 AA.

PRT;

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MEDLINE-21275466; PubMed-11381032;
Footz T.K., Brinkman-Mills P., Banting G.S., Maier S.A., Riazi A.M.,
Bridqland L.J., Hu S., Birren B., Minoshima S., Shimizu N., Pan H.,
Nguyen T., Fang F., Fu Y., Ray L., Wu H., Shaull S., Phan S., Yao Z.,
Chen F., Huan A., Hu P., Wang Q., Loh P., Qi S., Roe B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Analysis of the cat eye syndrome critical region in humans and the region of conserved syntemy in mice: a search for candidate genes at or near the human chromosome 22 pericentromere."; Genome Res. 11:1053-1070(2001).
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Solute carrier family 25, member 18.
                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                SA18_HUMAN
                                                                                                                                                                                                                                  SLC25A18
                                                                                                        09H1K4;
                                 RESULT 15
SA18_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229
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                                                                                                                     SEQUENCE OF 1-26 FROM N.A. MEDINE-89127131; PubMed=2851701; MEDLINE-89127131; PubMed=2851701; Maloy S.R.; Mert C.R., Maloy S.R.; Rent C.R.; Mergaliation of proline utilization in Salmonella typhimurium: melecular characterization of the put operon, and DNA sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
Multifunctional enzyme; Oxidoreductase; Flavoprotein; FAD; NAD;
Transcription regulation; Repressor; DNA-binding; Proline metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: IN THE N-TERMINAL SECTION; TO PROLINE DEHYDROGENASES. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CAUTION: Ref. 3 sequence differs from that shown due to a frameshift in position 1048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                      MOL. Gen. 213:125-133(1988).
-!- FUNCTION: OXIDIZES PROLINE TO GLUTAMATE FOR USE AS A CARBON AND NITROGEN SOURCE AND ALSO FUNCTION AS A TRANSCRIPTIONAL REPRESSOR
                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: L-proline + acceptor + H(2)0 = (S)-l-pyrroline-5-carboxylate + reduced acceptor.
-!- CATALYTIC ACTIVITY: 1-pyrroline-5-carboxylate + NAD(+) + H(2)0 =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- COFACTOR: FAD.
-1- PATHWAY: PROLINE UTILIZATION.
-1- INDUCTION: BY PROLINE, AUTOREPRESSION AND CATABOLITE REPRESSION,
-1- INDUCTION: BY PROLINE, AUTOREPRESSION.
AND IS POTEWTIALLY UTROGEN CONTROLLED.
AND IS POTEWTIALLY NATROGEN CONTROLLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 ALDEHYDE DEHYDROGENASE.

13 BY SIMILARITY.

17 BY SIMILARITY.

18 SIMILARITY.

19 A. R. IN REF. 1).

144089 MW; 6F38C93EE6A5FD4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROLINE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X70843; CAA50193.1; --
EMBL; AE008748; AAL20055.1; ALT_FRAME.
EMBL; X12569; CAA31081.1; ALT_SEQ.
PIR; S31910; S31910.
PIR; S31910; S31910.
StyGene; SG10321; putA.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR0020872; Pro_dh.
Wilson R.K.;
                                                                           Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-glutamate + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00171; aldedh; 1
Pfam; PF01619; Pro_dh; 1
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1320 AA;
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Mol. Gen. Genet. 21
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Matches 24; Conserv
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       Waterston R.,
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ACT_SITE
CONFLICT
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       RRARA 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 WELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNNLGFNEL--AGKASFAHSFVSG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 WRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANG-AAG 78
-! - SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  э;
Э;
                    inner membrane (By similarity).
-i- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B23A9E5036671634 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%; Score 74.5; DB 1; 28.0%; Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSTIE; PS00215; MITOCARRIER: 1.
Mitochondrion; Inner membrane; Repea
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                     EMBL; AY008285; AAG22855.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33848 MW;
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126
205
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106
185
225
288
315 AA;
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Best Local Similarity
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TRANSMEM
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Job time: 1241 sec

- NORSASGRAGMVQGLLQEFSLSSQEG 162 GNSHIANGAAGCVATLLHDAAMNPAEG 94

89 137

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 27, 2002, 04:19:23 ; Search time 130.92 Seconds (without alignments) 124.210 Million cell updates/sec Run on:

US-09-870-113-10 502 1 MOSLQPDPAARYRNVLEALW......GAAGCVATLLHDAAMNPAEG Title: Perfect score: Sequence:

94

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

562222 seqs, 172994929 residues Searched:

562222

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_19:* Database :

sp_archea:*
sp_archea:*
sp_fungi:*
sp_fungi:*
sp_human:*
sp_nnvertebrate:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:*
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sp_vortebrate:*
sp_vortebrate:*
sp_vortebrate:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SOMMAKIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	496	98.8	364	4	Q96A46	O96a46 homo sapien
7	351	6.69	347	4	Q9NYZ2	O9nvz2 homo sapien
m	348	69.3	338	11	092068	092098 mus musculu
4	280	55.8	155	4	096981	0969s1 homo sapien
S	276	55.0	182	1	Q912Y0	O912v0 mus musculu
9	216.5	43.1	312	'n	023125	023125 caenorhabdi
7	171.5	34.2	379	Ŋ	O9VAY3	O9vav3 drosophila
80	168	33.5	303	Ŋ	094638	094638 onchocerca
0	167.5	33.4	380	ß	O9NHY6	O9nhv6 drosophila
10	166	33.1	301	'n	094634	094634 onchocerca
11	135	26.9	781	10	09LMJ6	O91m16 arabidopsis
12	130.5	26.0	289	10	082049	082049 ribes nigru
13	130	25.9	331	10	064731	064731 arabidopsis
14	118	23.5	303	٣	014281	014281 schizosacch
15	115	22.9	320	11	Q921P8	O921p8 mus musculu
16	114	22.7	345	11	09CYJ1	Ogevii mus musculu

Q9bsk2 homo sapien Q27244 caenorhabdi Q9ax19 hoxdeum vul Q9wvf9 drosophila Q14589 homo sapien Q9ax03 oryza sativ Q9uhr1 homo sapien Q90x05 homo sapien Q95cq1 homo sapien Q95cq1 mus musculu Q95cq1 arabidopsis Q9syy5 arabidopsis Q94x32 arabidopsis Q94x32 arabidopsis Q9dam5 mus musculu Q9dam6 mus musculu Q9dam6 mus musculu Q9dam7 mus musculu Q9dam8 arabidopsis Q9dam8 arabidopsis Q9d88 mus musculu Q9bc74 homo sapien Q9bc74 homo sapien Q9bc71 homo sapien Q9bc71 homo sapien Q9bc71 homo sapien Q9bc71 homo sapien	Q9vq37 drosophila Q9545 drosophila Q18844 caenorhabdi Q9v105 drosophila Q9c6K8 arabidopsis
4 09BSK2 5 027244 0 029ARL9 4 014589 10 029AX03 10 029AX03 10 029AX03 11 02020 11 02020	5 09VQ37 5 095TJ5 5 018844 5 09VI05 10 09C6K8
321 384 4322 3322 3323 3313 311 3113 313 313 313	358 365 310 449 311
	17.5 17.5 17.4 17.2
80.0101 80.0000 80.000 80.000 80.000 80.000 80.000 80.000 80.000 80.0000 80.	88 88 87.5 86.5
1111 122222222222222222222222222222222	41 44 44 54 54

ALIGNMENTS

RESULT 1 09646 10 09646 PRELIMINARY; PRT; 364 AA. AC 09646 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) DE MITOCHONDRIAL RNA SPLICTNG PROTEIN 3/4 (PUTATIVE MITOCHONDRIAL SOLUTE DE CARRIER SPLICE VARIANT). GN HMR33/4. ON CBL TAXID=9606; RN [1] FAXID=9606; RN [1] F. Nikali K., Gregan J., Leibiger I., Leibiger B., Schweyen R., RA Li F., Nikali K., Gregan J., Leibiger I., Leibiger B., Schweyen R., RA Larson C., Suomalainen A.; RT "Characterization of a novel human putative mitochondrial transporter RT homologous to the yeast mitochondrial RNA splicing proteins 3 and 4."; RR "Characterization of a novel human putative mitochondrial transporter RDE. ABS. JAX49519.1; DR EMBL; AF327402; AAK49519.1; SQ SEQUENCE 364 AA; 39271 MW; 22049C4F8DD7AS77 CRC64; MATCHES 93; CONSELVATIVE ON MISMATCHES ON Indels 0; Gaps ON 1 MOSLOPDPAARYRNULDALMRITREGLMRPMRGINVTATGACPAHALYFACYEKIKFT, 190 DD NOSLOPADAARYRNULDALMRITREGLMRPMRGINVTATGACPAHALYFACYEKIKFT, 190 DD NOSLOPADAARYRNULDALMRITREGLMRPMRGINVTATGACPAHALYFACHERMRT, 190 DD NOSLOPADAARYRNULDALMRITREGLMRPMRGINNTATATGACPAHALYFACHERMRT, 190 DD NOSLOPADAARYRNULDALMRTTATTATICATHALMPT TRATECTHALMPT TRATECTHALMPT TRATECTHALMPT TRATECTHALMPT TRATECTHALMPT TRATECTHALMPT TRATECTHALMPT TRATECTHALMPT TRATECTHALMPT TRATECT
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RESULT **Q9NYZ2**

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STRAIN=C57BL/6J;
Li Q., Eckenrode S., Wang C., Ruan Q., Shi J., McIndoe R.A., She J.;
Li Q., Eckenrode S., Wang C., Ruan Q., Shi J., McIndoe R.A., She J.;
A novel mouse mitochondrial carrier protein gene is up-regulated from young to adult NOD mice.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF361699; AAL27990.1;
EMBL; AF361699; AAL27990.1;
SEQUENCE 182 AA, 19938 WW; 18E2C5E801228693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Li Q., Eckenrode S., Ruan Q., Wang C., Shi J., McIndoe R.A., She J.;
"Molecular cloning of a novel mictochondria solute carrier protein
(MSCP) gene from mouse and human and its down-regulation in mouse
spleen during the maturation of the immune system.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 155;
                                                                                                                                              Last sequence update)
Last annotation update)
PROTEIN (HYPOTHETICAL 16.8 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AX032628; AAK38154.1;
EMBL; BC0150113;
Hypothetical protein.
SEQUENCE 155 AA; 16832 MW; 8ACB98A483C8E6EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Pred. No. 1.2e-23;
                                                       155 AA
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MITOCHONDRIAL CARRIER-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=UTERUS, AND LEIOMYOSARCOMA;
                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, MITOCHONDRIA SOLUTE CARRIER
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Matches 50; Conservative
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Best Local Similarity
Matches 49; Conserv
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Q969S1;
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RESULT
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                                                              ID DDT TD DDT TD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
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                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRIAL SOLUTE CARRIER-LIKE PROFEIN.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A new gene which is highly expressed in NOD mice spleen.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288621; AAL23859.1; -. EMBL; AF288621; AAL23859.1; -. SEQUENCE 338 AA; 37510 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.9%; Score 351; DB 4; Length 347; 67.7%; Pred. No. 3.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Song H., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
"A novel gene expressed in human hypothalamus.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF223466; AAF64141.1;
InterPro: IPR001993; Mitoch_carrier.
Pfam; PF00153; Mitoch_carrier.
PROSITE; PS00215; ATTOCH_CARRIER; UNKNOWN.2.
SEQUENCE 347 AA; 37828 MW; 700DE61B230E001E CRC64;
                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                       Created)
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                                                    Q9NY22;
01-OCT-2000 (TIEMBLEEL 15,
01-OCT-2000 (TIEMBLEEL 15,
01-JUN-2001 (TIEMBLEEL 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 6/....
Frac 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.3%
Best Local Similarity 68.8%
Matches 64; Conservative
                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-HYPOTHALAMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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HT015.
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Worthan J.R., Richards S., Ashburner M., Henderson S.N.,

Brandon R.C., Rogers Y.-H.C. Blazej R.G., Champe M., Pfeiffer B.D.,

RA Britl J.F., Apbayani A. An H.-J., Andrews-Pfannkoch C.R., Baldwin D.,

Rallew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E.M.,

Rallew R.M., Basu A., Buller H.-J., Bhorktaroglu L., Beasley E.M.,

RA Burtis K.C., Busam D.A., Buller H., Cadler E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller R., Davenport L.B., Davies P.,

Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunk

RA Fosler C., Gabriellan A.E., Garg N.S., Galbart W.M., Classer K.,

Glodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Burtin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Classer K.,

Glodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Burtin M., Kalush F., Karpen G.H., Gu Z., Kennison J.A., Ketchum K.A.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J. R., Houck J.,

Busko P., Lei Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,

RA Liu X., Matlen B., Moritosh T.C., Mortis J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Murzny D.M., Nelson D.L.,

Relazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Shue B.C., Saden Kiamos I., Sanger E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

The genome sequence of Drosphila melanogaster.",

The genome sequence of Drosphila melanogaster.",

Rudor S. Brandling G.C., Turner R. Wang S., Zhu X., Salth H.O.,

The genome sequence of Drosphila melanog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Y, CN BW SP.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INNER MEMBRANE (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

EMBL, AE003763; AAF56764.1; -

EMBL, AY060268; AAL25307.1; -

FlyBase; F99n0039561; CG4963.

InterPro; IPR001999; Mitoch_carrier.

InterPro; IPR001097; Mitoch_carrier.

Pfam; PF00153; mito_carrier.

3.
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PROSITE; PS00215; MITOCH_CARRIER; 2.
Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 379 AA; 41794 MW; F6A20BABA35F5C2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.2%; Score 171.5; DB 5
40.9%; Pred. No. 4.8e-11;
ive 16; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::::|| |||:||| :|::::100 AKFTSVRNLNYVISGA---VATLIHDAISSPTD 129
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Best Local Similarity 40.95
Matches 38; Conservative
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                                                          Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 MQSLCPCPETKCPTPVHSLMSIVKREGWLRPLRGVNAVAAGSMPAHALYFTVYEKMKGYL 104
                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                             1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Swinburne J., Ainscough R.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating bloingy.";
Science 282:2012-2018(1998).
EMBL; 26521; CAA91399.1;
InterPro; IPR001993; Mitcoh_carrier.
Pfam; PF00153; mitco_carr; 3.
PROSITE; PS00215; MITCOH_CARRIER; UNKNOWN_2.
SEQUENCE 312 AA; 34093 MW; D65FC4DD2936F76A CRC64;
                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                          312 AA
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                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99069613; PubMed=9851916;
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50.08;
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                                                                                                                                                    PRELIMINARY;
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                                                                                                                       61 SDVIHPGGNSHIANG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
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Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                           W02B12.9 PROTEIN.
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NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                    01-NOV-1996
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SEQUENCE 1
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Gaps

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Indels

34; DB 5;

Length 379;

RESULT 09VAY3

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094638 094638;

RESULT 094638

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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu S.X., Chan A., Yu G., Etgu P., Lee J.M., Lenz C., Pham P., Sakano H., Toriumi M., Chung M., Goldsmith A., Liu A., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A., Hansen W., Johnson Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.; "The sequence of BAC Flokl from Arabidopsis thaliana chromosome 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                           42 MGSL--SPPTKNMNIVSTLRTMITREGLLRPIRGASAVVLGAGPTHSLYFAAYEMTKELT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catmull J., Miller D.J.;
"cDNAs from Onchocerca sp. encoding members of the MRS3/MRS4 class a mitochondrial solute carriers.";
EMBL; U45997; AAB19036.1; -...
Interpro; IPR001993; Mitoch_carrier.
PROSITE; PS002153; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 301 AA; 34176 MW; COBABD819FB8EA79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               Onchocerca gibsoni.
Sukaryota Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
NCBI_TaxID=6284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 301;
35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37; Indels
                                                                                                                                                                                                                                                                                             01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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  Mismatches
                                                                                                                                        ::::|| ||||:||| :|:
100 AKFTSVRNLNYVISGA---VATLIHDAISSPTD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
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                                                                                                                                                                                                                                                           301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=96326580; Pubmed=8703971;
16;
                                                                                                                                                                                                                                                                                                                                                             MITOCHONDRIAL SOLUTE CARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, FIDK1.26 PROTEIN.
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
37;
                                                                                                                                                                                                                                                                             094634
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Q9LMJ6
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                           MEDLINE-96326580; Pubmed-8703971; Catmull J., Miller D.J.; "cbNAs from Onchocerca sp. encoding members of the MRS3/MRS4 class of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.5%; Score 16%; DB 5; Length 30
36.6%; Pred. No. 9.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CANTON-S;
Schmid K.J., Tautz D.;
Schmid K.J., Tautz D.;
Schmid K.J., Tautz D.;
Schmid K.J., Tautz D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF211402; AAF73387.1;
FlyBase; FBgn0039561; CG4963.
InterPro; IPR001993; Mitcoh_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 303 AA; 33861 MW; 2249FA547E5D617C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41844 MW; 4C9AA524B97F8C6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 41.8 KDA PROTEIN.
                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 167.5; DB 5;
Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1282:179-181(1996).
EMBL; U45998; AAB19037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                             Created)
                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                             mitochondrial solute carriers.
                                                                                                                                                         MITOCHONDRIAL SOLUTE CARRIER. Onchocerca volvulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.4%;
39.8%;
                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                  (TrEMBLrel. 02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.5%
Best Local Similarity 36.6%
Matches 34; Conservative
                                                                                                                                                                                                                      Onchocerca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00153; mito_carr;
                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                        NCBI_TaxID=6282;
                                                                                                                                                                                                                      Onchocercidae;
                                                                                             01-FEB-1997
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                                                                                                                                                                                                                                                                                                        H.V.;
that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Saxifragales; Grossulariaceae; Ribes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                                                                                                                                                                                      Length 781;
                                                                                                                                                                                             Score 135; DB 10; Length 7
Pred. No. 1.4e-06;
4; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 1.4e-06;
17; Mismatches 35; Indels
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AG067971; AAR68217.1; --
InterPro; IPR001993; Mitch.Carrier.
InterPro; IPR002067; Mit.Carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00153; mito_carr; 3.
PROSTIE; PS00215; MITOCH_CARRIER; 2.
Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 289 AA; 30383 MW; 5666EAB03DCC507C CRC64;
                                                                           Pfam; PF00153; mito_carr; 4.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 781 AA; 87081 MW; 9FB579B9BD746D1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                       61 SDVIHPGG--NSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                         14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.0%; Score 130.5; 35.3%; Pred. No. 1.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289
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STRAIN-EV. BER ALDER; TISSUE-FRUIT;
Woodhead M.R.;
Thesis (1995), University of Dundee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, La. MITOCHONDRIAL CARRIER PROTEIN.
                                                                                                                                                                                                 26.98;
38.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 08, TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 35.3% nes 30; Conservative
                                                                                                                                                                                                 Query Match 26.99
Best Local Similarity 38.99
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=78511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribes nigrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998
01-DEC-2001
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082049;
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STRAIN-CV. COLUMNIA;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Evjii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                             Arabidopsis thaliana (Mouse-ear cress). Bubryophyta; Tracheophyta; Bukaryots; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 MOALRSCP-IKPIGIROAFRSIIKTDGPSALYRGIWAMGLGAGPAHAVYFSFYEVSKKFL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC004165; AAC16956.1; -.
InterPro; IPR001993; Mitoch_carrier. Pfam; PF00153; Mito_carrisr. Profo153; Mito_carrisr. Browsite; PS00215; MITOCH.CARRIER; UNKNOWN 2. SEQUENCE 331 AA; 35961 WW; A0DE93084BBC8BC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.9%; Score 130; DB 10; 37.9%; Pred. No. 1.9e-06; Live 15; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDVIHPGG--NSHIANGAAGCVATLLHDAAMNPAE 93
331
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                                                                                                               PUTATIVE MITOCHONDRIAL CARRIER PROTEIN
                                         07, Created)
07, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 37.9%;
.....hes 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
                                            (TrEMBLrel.
                                                                     (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
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                                         01-AUG-1998
01-AUG-1998
                                                                                           01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001
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Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thaliana
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                                                                                                                                                                                                                                                                                                                                                          60 NIVNSVIKISSTEGVYSLWRGISSVIMGAGPSHAIYFSVLEFFKSK---INASPDRPLA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                       14 NVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPG 67
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 5730438N18 GENE.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musculariandologo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                             4;
           INNER MEMBRANE (BY SIMILARITY).

-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

EMBL, 299168; CAB16300.1, -

Interpro; IPR001993; Mitoch_carrier.

Pfam; PF00153; mito_carris.

Hypothetical protein; Mitoch_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 22.9%; Score 115; DB 11; Length 320; Best Local Similarity 32.9%; Pred. No. 8.5e-05; Matches 28; Conservative 12; Mismatches 41; Indels
                                                                                                                                                                                                                                                                          Query Match 23.5%; Score 118; DB 3; Length 303;
Best Local Similarity 33.3%; Pred. No. 3.7e-05;
Matches 26; Conservative 17; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011293; AAH11293.1; - SEQUENCE 320 AA; 35050 MW; F40B5912706583CD CRC64;
                                                                                                                                                                                                                                69975CDE18107AB5 CRC64;
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116 SALAGACAITISDAFMTP 133
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                                                                                                                                         Transport.
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81
117
164
208
303 AA;
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SEQUENCE FROM N.A.
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Human mitochondria
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Human polypeptide
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1 MQSLQPDPAARYRNVLEALW......QFAEESTSVLVGNSVTLFYH 131
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                747574 segs, 111073796 residues
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Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
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AAM79039
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AAM41505
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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immune/h currant R dopsis th phila mel dopsis th polypept polypept polypept secreted	Arabidopsis thalia Human URCK ORE2547 Arabidopsis thalia
AAM85891 AAW17054 AAW17054 AAG22079 AAG22078 AAG22077 AAG3092 AAG43092 AAG43092 AAG69108 AAG69171 AAG69171 AAG69301 AAB930173 AAM40959 AAM40959 AAM40959 AAM40959	AAAL) 5360 AAGS0519 AAGS0518 AAGS0518 AAGS0517 AAGS0517 AAGS0517 AAGS0517 AAGS0517 AAGS0517 AAGS0517 AAGS0517 AAGS0517 AAGS0517 AAGS0517 AAGS0517 AAGS0517
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22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

	289 AA.	
	Protein;	
	standard;	
JLT 1 50383	AAB50383	AAB50383;

ALIGNMENTS

(first entry) 12-MAR-2001

Human uncoupling protein #6.

Human; uncoupling protein; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cardiant; vasotropic; cerebroprotective; neuroprotective, antibacterial; opthalmological; gastrointestinal; nephrotropic; gynaecological; vulnerary; thrombolytic; gene therapy; cancer; wound; infectious disease; thrombosis; arthritis; infertility.

Homo sapiens.

WO200061614-A2

19-OCT-2000

06-APR-2000; 2000WO-US09534

99US-0128701. 99US-0142821. 99US-0149448. 99US-0164751. 09-APR-1999; 08-JUL-1999;

12-NOV-1999;

(HUMA-) HUMAN GENOME SCI INC

Human bone marrow Novel human secret Human ORFX ORF2730 Drosophila melanog

AAU29748 AAB42966 ABB61130

AAM00938

Soppet DR; Rosen CA, Ni J, Komatsoulis G, Ruben SM,

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The present invention provides the protein and coding sequences for 43 movel human transport proteins (designated TPPF3). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative
        Page 133-134; 165pp; English.
                                                                              disorders such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-442253/47.
                                                                                                                                                  Best Local Similarity
Matches 98; Conser
                                                                                                     289 AA;
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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09-JUL-2000;
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                                                                                                        Sequence
                                                                                                                                         Query Match
            Claim
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                                                                                                     The present sequence is a human uncoupling protein. The nucleotide sequences encoding the uncoupling proteins may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder;
                                                                                                                                                  or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide with a human transport protein sequence is useful for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular systems
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                                                                                                                                                                                                                                                                                                           1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                  Uncoupling proteins and nucleic acid sequences encoding them, useful for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders -
                                                                                                                                                                                                                                                                                                                                  84
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9
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Au-Young J, Patterson
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Pred. No. 5.5e-51;
1; Mismatches 7;
                                                                                Claim 11; Page 323-324; 343pp; English.
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Lu DAM,
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Best Local Similarity 87.5%;
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune disorder; cancer
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N-PSDB; AAF27733.
  2000-656322/63.
                                                                                                                                                                                                                           289 AA;
            N-PSDB; AAC90457
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10-AUG-1999;
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28-OCT-1999;
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                                           Gaps
                                                                                  1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPWRGLNVTATGAGPAHALYFACYEKLKKTL 60
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                                                                                                            25 mgslqpdpaaryrnvlealwriirteglwrpmrglnvtatgagpahalyfacyeklkktl 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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                                                                                                                                                                                               Length 289;
                                           Indels
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Yang Y,
Score 505; DB 22;
Pred. No. 5.5e-51;
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iu C, Xue AJ,
    Drmanac RT;
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                                           1; Mismatches
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Wang Z, Wehrman T, Xu C,
Zhou P, Goodrich R, Drman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 6436.
                                                                                                                                                                                                                                                                                                                                       AAM41505 standard; Protein; 318
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2000US-0552317.
2000US-0598042.
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2000US-0653450.
2000US-0662191.
2000US-0693036.
72.7%;
llarity 87.5%;
Conservative
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WPI; 2001-442253/47.
N-PSDB; AAI58875.
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15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
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          the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                       system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, anyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, estivation in activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, among and thrombolytic activity, accepting and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang D;
                                                                                                                                                                                                                                                                                                   54 mqslqpdpaaryrnvlealwriirteglwrpmrglnvtatgagpahalyfacyeklkktl 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; hardneric; amyotrophic lateral sclerosis; Shy-Brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                                                                                                                                                             1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F, Warng J;
                                                                                                                                                                                                                                                                                         61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSC 106
                                                                                                                                                                                                                                                                                                                                      Score 505; DB 22; Length 318; Pred. No. 6.2e-51; 1; Mismatches 7; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asundi V, Chen R, Ma Y,
Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                        AAM39719 standard; Protein; 268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 2864.
                                                                                                                                                                                                                                72.78;
87.58;
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0620312.
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2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                        Best Local Similarity 87.5 Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
Wang Z,
Zhou P,
                                                                                                                                                                                              318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                   C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-2000;
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19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000;
14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukaemia.
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Zhao QA,
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                AAM39719;
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                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                    system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activity,inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 mhslqsdpagryrnvlevlwriirteglwrpmrglnvtatgawpahalyfacyeklkktl 63
useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.5%; Score 476; DB 22; Length 268; 83.0%; Pred. No. 1.3e-47; Live 1; Mismatches 12; Indels (
                                                                                                             Example 4; SEQ ID NO 2864; 10078pp; English.
Novel nucleic acids and polypeptides, us
such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM79039 standard; Protein; 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein SEQ ID NO 1701.
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2000US-0663561.
2000US-0693325.
2000US-0728422.
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2000US-0598075.
2000US-0620325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.v.,
-hos 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US04098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 AA;
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Leach M;

(CURA-) CURAGEN CORP.

us-09-870-113-12.rag

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Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 4662-4663; 5507pp; English.
                                                                                                    31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                             31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                         WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC77189
                                                                                                                                                                                                                                                                Shimkets RA,
                    05-0CT-2000
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                                                                                                                                                                                                                                                                                                     The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunositmulant; thrombolytic; coaqulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiantanaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency, malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coaqulation;
                                         χ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                           Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                      Xu C, Cao Y,
R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ORFX ORF2744 polypeptide sequence SEQ ID NO:5488.
                                    Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P,
Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.6%; Score 352; DB 22;
68.8%; Pred. No. 6.1e-33;
ative 12; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                              Claim 20; Page 4043; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB42980 standard; Protein; 272 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Conservative
                                                                                                                           WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 AA;
(HYSE-) HYSEQ INC
                                                                                                                                                  N-PSDB; AAK52172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation.
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
contingentiatic; antiparkinsonian; nootropic; neuroprotective;
coteopathic; anticonvulsant; antiarthritic; immunosuppressant;
immunostimulant; cardiant; thrombolytic; coapulant; vasotropic;
contidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunosuppressive;
contidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunosuppressive;
contidiabetic; hypotensive; dermatological; immunosuppressive;
antidification and antidanement. The sequences can be used for determining
the presence of or predisposition to, or preventing or treating
the presence of or predisposition to, or preventing or treating
the proteins and nucleic acids may be used to treat cancers,
coliferative disorders, neurodegenerative disorders, osteoarthritis,
coliferative disorders, neurodegenerative disorders systemic lupus
crythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
bacterial or fungal infection, malaria, autoimmune disorders, asthma,
allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human mitochondrial solute carrier protein; hMSC-o; hypothalamus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB60658 standard; Protein; 331 AA
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Best Local Similarity 67.79
Watches 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 AA;
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thrombosis; contraceptive

WO200058473-A2

Homo sapiens.

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Chen R,

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by a bone marrow-expressed polynucleotide. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous cor increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be cused as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, vaccination, gene therapy, nutritional supplement;
stem cell proliferation, haematopoiesis, nerve tissue regeneration;
immune suppression, immune stimulation, anti-inflammatory, leukaemia.
                                                                                                                                                                                                                                                        Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                Xue AJ, Yang Y, Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.5%; Score 351; DB 22; Length 366; 67.7%; Pred. No. 1.1e-32; Ive 13; Mismatches 17; Indels
                                                                                                                              Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
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                                                                                                                                                                                                                                                                                                           Claim 10; Page 504-505; 648pp; English.
                                                                                                                                Liu C,
                                                                                                                           Boyle BJ, Tang YT, Liu ang J, Werhman T, Xu C, Zhou P, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU29748 standard; Protein; 677
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
30-NOV-2000; 2000US-02505883.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                   WPI; 2001-488707/53.
N-PSDB; AAH90057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 AA;
                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200179449-A2.
                                                                                                                                                Wang
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                                                                                                                                              Ren F, We
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                              Ford JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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0
                                                                                                                                                                                                                                                                                                                                                                                                                 protein, hMSC-o (AAB60658), and cDNA encoding it (AAF59920). hMSC-o is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-o proteins and nucleic acids, and the detection of hMSC-o proteins and nucleic acids in a sample. The present sequence represents hMSC-o.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                          New human mitochondrion solute carrier protein and its nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                  relates to a novel human mitochondrial solute carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antityrial; antibacterial; antifungal; anti-HTV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human immunodeficiency virus; HIV; autoimmune disorder; haemophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 351; DB 22;
Pred. No. 9.2e-33;
                                                                                                                                                                                                 (SREN-) SOUTHERN RES CENT NAT HUMAN GENE GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bone marrow protein, SEQ ID NO: 414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM00938 standard; Protein; 366 AA.
                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 20; 21pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                         17-MAR-2000; 2000CN-0114958
                                                                                                                                                             17-MAR-2000; 2000CN-0114958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-2000; 2000WO-US34960.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Conservative
                                                                                                                                                                                                                                     Gao X, Xiao H;
                                                                                                                                                                                                                                                                       WPI; 2001-050544/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 AA;
                                                                                                                                                                                                                                                                                          N-PSDB; AAF59920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200153453-A2
                                                                                                                                                                                                                                                                                                                                                                                                The invention
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                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                   CN1269409-A.
                                                                                       11-0CT-2000.
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                                                                                                                                                                                                                                     Zhang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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AAM00938

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Gaps

99US-0127636 99US-0127728

Leach M;

99US-0127607

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Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 4641; 5507pp; English.
                                                                            31-MAR-2000; 2000WO-US08621
                                                                                                                                                            30-MAR-2000; 2000US-0540763
                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                               2000-602362/57.
                                                                                                                                                                                                                                                                                N-PSDB; AAC77175
             WO200058473-A2.
                                                                                                                                                                                                                               Shimkets RA,
                                                                                                              31-MAR-1999;
                                                                                                                                               05-APR-1999;
                                                                                                                                 02-APR-1999;
                                              05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying at therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. They may be used to increase stem cell proliferation; to regulate hemmatopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUS510-AAU3304 represent the amino acid in treatment of leukaemias. AAUS510-AAU3304 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticorvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; prolliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; ohlosterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                               Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MOSLOPDPAARYRNVLEALWRIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 46.3%; Score 322; DB 22; Length 677; Best Local Similarity 63.4%; Pred. No. 6.3e-29; Matches 59; Conservative 13; Mismatches 21; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX ORF2730 polypeptide sequence SEQ ID NO:5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                 Claim 20; Page 189; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB42966 standard; Protein; 155 AA
                                                                Drmanac RT
26-JAN-2001; 2001US-0770160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-FEB-2001 (first entry)
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                                                                                               WPI; 2001-611725/70.
                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              677 AA;
                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                               Tang YT,
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; heuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; and antidanematic; antidiabetic medicious or determining the proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, chypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, and proteins and proteins and antidary and antidary and cartifiane and antidary and cartificative disorders, astimate, and antidary and cartificate and ant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.7%; Score 276; DB 21;
64.0%; Pred. No. 2.3e-24;
tive 13; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB61130 standard; Protein; 379 AA.
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133 ndvfhhqgnshlang 147
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2000US-0190076
           17-JAN-2001; 2001WO-US01354
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14-AUG-2000;
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14-AUG-2000;
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14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
33-AUG-2000;
31-SEP-2000;
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14-SEP-2000;
21-SEP-2000;
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18-APR-2000;
19-MAY-2000;
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05-SEP-2000;
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4-SEP-2000;
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   3,
                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                        ch 25.7%; Score 178.5; DB 22; Length 379;
1 Similarity 39.3%; Pred. No. 2.4e-12;
44; Conservative 17; Mismatches 40; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 10182; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune/haematopoietic antigen SEQ ID NO:13484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM85891 standard; Protein; 59
                                                                                                                                                             Li PWD,
                                                                                       23-MAR-2001; 2001WO-US09231.
                                                                                                           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                              Drosophila melanogaster
                                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 44; Conserva
                                                                                                                                                                               WPI; 2001-656860/75.
N-PSDB; ABL05233.
                                                                                                                                        (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                            379 AA;
                                                 WO200171042-A2
                                                                                                                                                                                                                                 interactions -
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          pharmaceutical
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                                                                   27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

metastasis

Claim 11; SEQ ID NO 13484; 3071pp + Sequence Listing; English.

AMX54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
corrections and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
correct the activity of (I) by expressing inactive proteins or to
that affect the activity of (I) by expressing inactive proteins or to
coppuncteotides may be used to production of (I). Additionally, (I)
coplynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
coptent. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
concers and cancer metastases of haematopoietic antigen genomic
cancers and cancer metastases of haematopoietic antigen genomic
cancers from the present invention. AAK54942 to AAK54950 and AAM82169
represent sequences used in the exemplification of the present invention.

1;

Sequence

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Ruben SM;
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RIB polypeptides (AAW17050-54) are encoded by cDNA clones (AAT68953-
                                                   8 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated promoters from blackcurrant fruit - used for driving fruit-specific expression of DNA sequences in transgenic blackcurrant and other non-climacteric fruit
                          11;
                                                                                                                                                                                                                                         Blackcurrant; fruit-specific promoter; RIB7; transgenic plant.
23.8%; Score 165.5; DB 22; Length 59; 59.3%; Pred. No. 6.6e-12; Live 1; Mismatches 12; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                    Brennan RM, Taylor MA, Woodhead MR;
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                                                                                                                                        AAW17054 standard; Protein; 289 AA
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                                                                                                                                                                                                               Blackcurrant RIB7 polypeptide.
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N-PSDB; AAT68957.
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    3;
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                                                                                                                                                 69 NSHIANGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSCTCISLQFAEESTSVLV 122
                                                                                                          Gaps
57) that exhibit differential expression in blackcurrant fruit during the ripening period of fruit development. RIB7 shows case similarity to yeast MRS4, a yeast mitochondrial RNA splicing protein. RIB7 is expressed almost entirely in fruit. The promoter region (AAT68952) of the RIB7 gene can be used as a fruit-specific promoter.
                                                                             20.4%; Score 141.5; DB 18; Length 289; 31.2%; Pred. No. 3.8e-08; Live 18; Mismatches 51; Indels 19;
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990x-0161361.
990x-0161920.
990x-0161993.
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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Search completed: August 27, 2002, 03:56:01 Job time: 4913 sec

Sequence 2, Appl. Sequence 10, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 4, Appl. Sequence 14, Appl. Sequence 14, Appl. Sequence 14, Appl. Sequence 17, Appl. Sequence 17, Appl.

Sequence 33, Sequence 4, 7

Sequence Sednence sequence 13, Appl Sequence 2, Appli

ALIGNMENTS

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COMPUTER: LINEAR COMPUTER: DEC COMPUTER: DEC COMPUTER: DEC COMPUTER: PATENTIN Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                             US-09-068-140A-10
Sequence 10, Application US/09068140A
Sequence 10, 284109
GENERAL INFORMATION:
APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
APPLICANT: and Rex Michael Brennan
TITLE OF INVENTION: Blackcurrant Promoters and Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                 US-08-718-388-9
US-08-718-388-9
US-09-160-119-4
US-09-160-119-4
US-08-961-871-10
US-08-977-466-2
US-09-172-528-2
US-09-172-528-2
US-09-503-579-2
US-09-503-579-2
US-09-268-140-4
US-08-053-171-14
US-08-053-171-14
US-08-053-171-17
US-08-053-171-17
US-08-915-190A-13
                                                                                                                                                                                                                                                                                                                                        ...orESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: NO. 6221409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10:
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ 1D NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Ribes nigrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: unknown TOPOLOGY: unknown
432
5594
5405
311
447
647
647
308
308
308
308
1119
1119
1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; STRAIN: Ben Alder
US-09-068-140A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: NORIGINAL SOURCE:
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Sequence 10, Appl
Sequence 15, Appl
Sequence 19, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 12, Appli
                                                                      August 27, 2002, 03:58:53; Search time 48.11 Seconds (Without alignments) 66.509 Million cell updates/sec
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Sequence 2, A
Sequence 5, A
                                                                                                                   US-09-870-113-12
695
1 MQSLQPDPAARYRNVLEALW......QFAEESTSVLVGNSVTLFYH 131
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Sequence
Sequence
Sequence
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Compugen Ltd
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US-09-068-140A-15

US-08-933-750C-19

US-08-933-750C-19

US-09-234-613-12

US-09-128-721-14

US-08-128-721-12

US-08-128-721-12

US-09-268-347-32

US-09-268-347-32

US-09-268-347-32

US-08-995-11

US-08-995-11

US-08-995-12

US-08-995-2

US-09-268-347-44

US-09-268-347-44

US-09-28-347-44
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         GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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141.5
94.5
94.5
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69 NSHIANGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSCTCISLQFAEESTSVLV 122
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                                          9 AARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG 68
  19:
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  51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corely, Neil C.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: LDW COMPTON DOS SOFTWARE: FASTESO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/933,750C FILING DATE: SEPLEMBER 23, 1997
  40; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0356 US
                                                                                                                                                                                                                                                                                                                                                ; Sequence 19, Application US/08933750C; Patent No. 5932442; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                              Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 351 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.69
Best Local Similarity 29.69
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LIBRARY: SYNOOAT01; CLONE: 724157
US-08-933-750C-19
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                                                                                                                                                                                                           123 GNSVTLFY 130
                                                                                                                                                                                                                                               178 EEGIGAFY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                              9 AARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG 68
                                                                                                                                               20.4%; Score 141.5; DB 4; Length 289; 31.2%; Pred. No. 3.3e-09; live 18; Mismatches 51; Indels 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 141.5; DB 4; Length 328; Pred. No. 3.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,140A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex Michael Brennan TITLE OF INVENTION: Blackcurrant Promoters and Genes CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: NO. 6221409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70237
TELEPHONE: 610-270-5017
TELEPHONE: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                         US-09-068-140A-15
Sequence 15, Application US/09068140A
Patent No. 6281409
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.4%;
Best Local Simularity 31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 328 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Ribes nigrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; STRAIN: Ben Alder
US-09-068-140A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             139 EEGIGAFY 146
                                                                                                                                                                                                                                                                                       123 GNSVTLFY 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                              Matches
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64 IHPGG------NSH-IANGAAGCVATLLHDAAMNP------AEGND---SSTYHSV 103
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148 ALTSDLYAP------MVAGALARLGTVTVISPLELMRTKLQAQHVSYRELGAC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.9%; Score 90; DB 2; Length 320; Best Local Similarity 24.6%; Pred. No. 0.0074; Matches 30; Conservative 25; Mismatches 33; Indels
                                                                                                                                                                                                                                                     APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Cocley, Neal J.
APPLICANT: Corley, Neal C.
TITLE OF INVENTION: HOWAN REGULATORY MOLECULES
CORRESPONDENCES: 98
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/933,750C FILING DATE: September 23, 1997 CLASSIFICATION: 536
                                                                                                  Sequence 12, Application US/08933750C Patent No. 5932442 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                   APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer
APPLICANT: Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
                                                                                                                                                                                       APPLICANT: Hiliman, Jer
APPLICANT: Bandman, Old
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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CLONE: 207452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                RESULT 5
US-08-933-750C-12
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US-08-933-750C-12
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GT 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 GS 105
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                        92 DP-TRFTGTMDAFVKIVRHEGTRTLM---SGLPATLVMTVPATAIXFTAYDQLKAFLCGR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 DP-TRFTGTMDAFVKIVRHEGTRTLM---SGLPATLVMTVPATAIYFTAYDQLKAFLCGR 147
7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTL--- 60
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                                                                                                             61 ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSC 106
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                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hilman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: APPLICANT: APPLICANT: APPLICANT: Yue, Henry
APPLICANT: Cuegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVATION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF-0356 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 Sequence 19, Application US/09234613
Patent No. 6132973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BILLINGS, LUCY J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 351 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
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CLONE: 724157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
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US-09-234-613-19
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51 ACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEGNDSSTYHSVGSCTCIS 110
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                                                                                                                                                                                                                                                            ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYPES Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/628,291
                                                           APPLICANT: RYAN, THOMAS J.
APPLICANT: RYAN, THOMAS J.
APPLICANT: RYAO, THOMAS J.
APPLICANT: YAO, FONG
APPLICANT: RYAO, THOMAS APPLICANT
APPLICANT: RYAO, HARGRAVE, DEVANS & DOYLE LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09128722;
Patent No. 5962335;
GENERAL INFORMATION:
APPLICANT: Galivan, John H
APPLICANT: Yao, Rong
APPLICANT: Nimec, Zenia
TITLE OF INVENTION: Gamma Glutamyl Hydrolase;
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Jaeckle Fleischmann & Mugel, LLP
39 State Street
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; Sequence 4, Application US/08628291
; Patent No. 5801031
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/CDCKET NUMBER: 2089
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: protein
US-08-628-291-4
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TTTY: Rochester
                                                                                                                                                                                                                                          USA
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US-09-128-722-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.9%; Score 90; DB 4; Length 320; Best Local Similarity 24.6%; Pred. No. 0.0074; Matches 30; Conservative 25; Mismatches 33; Indels
                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
                                                                                                                                                                                                                                                                                                       STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
FILING DATE: September 23, 1997
APTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                 APPLICANT: Lal, Preeti
APPLICANT: Hilman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Tan, Purvi
APPLICANT: Tue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
                                           Sequence 12, Application US/09234613 Patent No. 6132973 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 320 amino acids TYPE: amino acid STRANDEDNESS: single TOPLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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; CLONE: 207452
US-09-234-613-12
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                    US-09-234-613-12
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

14614-1310 New York

COUNTRY:

STATE:

|: GT 164

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51 ACYEKLKKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMNPAEGNDSSTYHSVGSCTCIS 110
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                                                                                                                                                                                                                                                   Query Match 11.4%; Score 79; DB 1; Length 317; Best Local Similarity 32.4%; Pred. No. 0.16; Matches 24; Conservative 13; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/09128722
Patent No. 5962235
GENERAL INFORMATION:
APPLICANT: Galivan, John H
APPLICANT: Ryan, Thomas J
APPLICANT: Name, Zenia
TITLE OF INVENTION: Gamma Glutamyl Hydrolase
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Jaeckle Fleischmann & Mugel,
39 State Street
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F.R: 87681.98R196
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/09/128,722
FILING DATE: 04-AUG-1998
CLASSIFICATION: 514
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/628,291
FLING DATE: 05-APR-1996
ATTORNEY AGENT INFORMATION:
NAME: Braman, Susan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION:
                                                           not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              not relevant
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LENGTH: 317 amino acid
TYPE: amino acid
LENGTH: 317 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.4%
Best Local Similarity 32.4%
Matches 24; Conservative
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TELEPHONE: 710-262-4133
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MOLECULE TYPE: protein
US-09-128-722-12
                                                                                                                           ; MOLECULE TYPE: protein US-08-628-291-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 L----EELSVLVSN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 LOFAEESTSVLVGN 124
                          TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rochester STATE: New York
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Best Local Similarity 32.4%; Pred. No. 0.14;
Matches 24; Conservative 13; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INCORMATION:
APPLICANT: GALIVAN, JOHN H.
APPLICANT: RYAN, THOMAS J.
APPLICANT: RYAN, THOMAS J.
APPLICANT: NUMEC, ZENIA
TITLE OF INVENTION: GAMMA GLUTAMYL HYDROLASE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
COUNTRY: USA
                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/128,722 FILING DATE: 04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,291
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 12, Application US/08628291
; Patent No. 5801031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 2089,
TELECOMMUNICATION INFORMATION:
TELEFAX: 716-263-1636
TELEFAX: 716-263-1636
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 14603
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 LQFAEESTSVLVGN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 L----EELSVLVSN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-628-291-12
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INFORMATION FOR SEQ ID NO:
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                                                 LENGTH:
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                                                                                                                                                                                                                                                                                        APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VET. 2.0
|: ||: | | : | | : | | : | | : | | : | | 150 GVQVTSTSENGKHAITFALAKDLDMRTATVSDTLTIGGSTTTGSSTTPKVNVTSTASGLN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 GLNVTATGAGPAHALYFACYEKL---KKTLSDVIHPGGNSHIANGAAGCVATLLHDAAMN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 1094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 PAEG----NDSSTYHSVGSCTCISLQFAEESTSV---LVGNSVT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 FAKGATGANGDITVHLINIAS--TLQDILLINTGVVSKLDGNGIT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,135 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENISE DRIVE CITY: HILLSBOROUGH STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 10.2%; Score 71; DB 4 Best Local Similarity 27.9%; Pred. No. 8.7; Matches 29; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tessier-Lavigne, Marc
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
TITLE OF INVENTION: Semaphorin Receptors
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UC97-288-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                         Sequence 32, Application US/09268347 Patent No. 6335182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-936-135-4
; Sequence 4, Application US/08936135
; Patent No. 6054293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN. RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET UNMER: UC97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Haemophilus influenzae US-09-268-347-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
                                                                                              136 L----EELSVLVSN 145
                                                                  111 LOFAEESTSVLVGN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 32
LENGTH: 1094
                                                                                                                                                                                                      -09-268-347-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Median, David
APPLICANT: Regain, David
APPLICANT: Method and Composition for Weight Reduction
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Watov & Kipnes, P.C.
STREET: 186 Princeton-Hightstown Rd, PO Box 247
CITY: Princeton Junction
STATE: New Jersey
                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 2584; 29;
                                                                                                                                                                                                                                                                                                                                                                         35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Cassard, A.M. et al. publication OTHER INFORMATION: Genbank - Locus 37607
PUBLICATION INFORMATION:
AUTHORS: Cassard, A.M. et al.
TILE: Human Uncoupling Protein Gene: Structure, PCT-US94-09799-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette, 3.50 inch, 800 Kb storage
                                                                                                                                                                                          Query Match
10.2%; Score 71; DB
Best Local Similarity 29.1%; Pred. No. 29;
Matches 32; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS 6.0
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09799
FILING DATE: 29-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 29-AUG-1994
CLASSIFICATION
PROR APPLICATION DATA:
APPLICATION NUMBER: 08/249,179
FILING DATE: 25 May 1994
APPLICATION NUMBER: 08/144,313
FILING DATE: 30 AUGUST 1993
ATTORNEY AGENT INFORMATION:
NAME: Kipnes, Allen R.
REGISTRATION NUMBER: 28,433
REFERENCE/DOOKET NUMBER: 489.1.06
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION INFORMATION:
TELEFRANE: 609-243-0330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
PCT-US94-09799-1
; Sequence 1, Application PC/TUS9409799
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 609-275-1010
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                    2584 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL TYPE: Brown adipose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 306 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 08550
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: IBM
SEQUENCE CHARACTERISTICS
                             TYPE: A MAIN OF STRANDEDNESS: SINGle
TOPOLOGY: linear
WOLECULE TYPE: peptide
US-08-936-135-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: Human
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APPLICANT: Emanuel, Beverly S.
APPLICANT: Emanuel, Beverly S.
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
APPLICANT: Roe, Bruce
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5935783ris, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 QTSPNPKYRGFFHGVREIVREQGLKGTYQGLTATVLKQGSNQAIRFFVMTSLRNWYRGDN 213
                                                           Gaps
                                                                                                                                           243 PPGQYKSVPNCAMKVFINEGPTAFFKGLVPSFLRLGSWNVIMFVCFEQLKRELS 296
                                                         ö
                                                                                                      8 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLS 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 311;
Query Match 9.9%; Score 69; DB 5; Length 306; Best Local Similarity 27.8%; Pred. No. 2.5; Matches 15; Conservative 12; Mismatches 27; Indels
                                                         27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY: 1.7.

COUNTY: 1.8.

ZIP: 19103.

ZIP: 19103.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FLING DATE: 27-DEC-1996
CLASSIFICATION: 435
ATONREY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/POCKET UNBER: 35,719
REFERENCE/POCKET UNBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
9.9%; Score 68.5; DB 2;
Best Local Similarity 24.3%; Pred. No. 3;
Matches 27; Conservative 14; Mismatches 59;
                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/08775009 Patent No. 5935783 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-09-142-565-2
; Sequence 2, Application US/09142565A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-775-009-32
                                                                                                                                                                                                                                                  RESULT 14
US-08-775-009-32
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APPLICANT: Lee James Beeley
APPLICANT: Lee James Beeley
APPLICANT: Lee James
APPLICANT: Kelly Paine
APPLICANT: Kelly Paine
APPLICANT: Relly Paine
FILE REPERENCE: GH-30002
CURRENT APPLICATION NUMBER: US/09/142,565A
CURRENT FILING DATE: 1999-06-30
ERALIER FILING DATE: 1997-03-05
ERALIER FILING DATE: 1997-03-05
ERALIER FILING DATE: 1997-07-16
ERALIER FILING DATE: 1997-07-16
ERALIER FILING DATE: 1997-07-16
ERALIER FILING DATE: 1997-07-16
ERALIER APPLICATION NUMBER: 97305305.1
ERALIER FILING DATE: 1997-07-16
SEQ ID NOS: 6
SERRITER FILING SERVENTE SERV
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5

Search completed: August 27, 2002, 03:58:54 Job time: 4896 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

August 27, 2002, 03:57:43; Search time 80.04 Seconds (without alignments) 157.268 Million cell updates/sec

US-09-870-113-12 695 Title: Perfect score:

1 MOSLQPDPAARYRNVLEALW.....QFAEESTSVLVGNSVTLFYH 131 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues Searched:

283138

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description	hypothetical prote		റ	mtRNA splice defec		mtRNA splice defec	probable carrier p	hypothetical prote		hypothetical prote		Btl protein precur	probable mitochond	mitochondrial phos	hypothetical prote	O	probable carrier p	hypothetical prote	probable mitochond	allophycocyanin be	probable mitochond	phosphate transpor	allophycocyanin be	allophycocyanin be	adenylate transloc	allophycocyanin 1	2-oxoqlutarate/mal	mitochondrial carr	allophycocyanin be
SUMMARIES		6	2	2	6	6	3	7	0	o	٠ ٣	æ	6	3	1	6	œ	9	0	3		3	2	2	4	0	J.	S	σ	
SU	Ð	T2608	A86205	T00582	S55179	T39149	S1353	S44092	B96830	S60949	D84613	T4349	JQ1459	G86383	T4928	T20229	D84798	S57116	T23170	T51393	AFKKB	T18253	T51595	B44462	S33624	T05350	C31385	A36305	T5015	AFMWB
	DB	7	~	~	~	~	~	1	7	~	~	7	7	ď	~	7	7	7	7	7	-	7	7	7	~	~	~	7	~	Н
	Length	312	781	331	314	303	304	384	296	307	313	351	436	311	363	310	348	322	296	353	161	284	288	161	161	392	162	314	371	161
ф	Query	31.2	20.6	20.0	18.1	17.1	15.3	14.6	13.7	13.7	13.6	13.6	13.4	12.9	12.9		12.8	12.4	12.1		11.9	11.9	11.9		11.9	•	11.6	11.6		11.4
	Score	216.5	143.5	139	125.5	119	106	101.5	95	95	94.5	•	93	90	06	88	68		æ	83.5		83	æ	82.5		œ	80.5		œ	79.5
	Result No.	П	7	m	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

2-oxoglutarate car hypothetical prote Ca-dependent solut	allophycocyanin be formamidopyrimidin uncoupling protein	formamidopyrimidin hypothetical prote hypothetical prote		P	hypothetical prote hypothetical prote
A56650 T19322 T47703	AFKTB A12615 T05577	H97397 T01839 T45934	S64589 S31935 A82797	D82599 E69118	S54524 H86231
000	122	000	212	0.0	7 7
314 328 332	161 298 313	325 336 358	366 301 941	941 325	368 454
11.4	11.3	11.3	11.2	11.2	11.1
79.5	78.5 78.5 78.5	78.5 78.5 78.5	78 77.5 77.5	77.5	77
30 31 32	334 354	36 37 38	39 40 41	42	44

ALIGNMENTS

RESOLT 1 T26089 Hypothetical protein W02B12.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: T2008 C;Accession: T20089 R;Swinburne, J.; Ainscough, R. submitted to the EMBL Data Library, October 1995 A;Reference number: Z20149 A;Accession: T26089 A;Status: preliminary; translated from GB/EMBL/DDBJ	A; Residues: 1-312 <wild A; Residues: 1-312 <wild A; Cross-references: EMBL: 266521; PIDN:CAA91399.1; GSPDB:GN00020; CESP:W02B12.9 A; Experimental source: clone W02B12 C; Genetics: A; Gene: CESP:W02B12.9</wild </wild 	A;Map position: 2 A;Introns: 18/3; 251/3; 286/3 C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology	Query Match 31.2%; Score 216.5; DB 2; Length 312; Best Local Similarity 50.0%; Pred. No. 3.6e-14; Matches 47; Conservative 16; Mismatches 28; Indels 3; Gaps 2;
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45 MQSLCPCPETKCPTPVHSLMSIVKREGWLRPLRGVNAVAAGSMPAHALYFTVYEKMKGYL 104 1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60 ŏ qq

61 SDVIHPGGNSH-IANGAAGCVATLLHDAAMNPAE 93 οy

g

C1 RESULT

Appothetical protein [imported] - Arabidopsis thaliana
C;Specias: Arabidopsis thaliana (mouse-ear cress)
C;Specias: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A66205
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, W.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719

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A; Rosidues: 1-314 < KAU?
A; Cross-references: EMBL:X80731; NID:g854542; PID:g854563
R; Schmidt, C.; Soeallner, T.; Schweyen, R.J.
Mol. Gen. Genet. 210, 145-152, 1987
A; Title: Nuclear suppression of a mitochondrial RNA splice defect: nucleotide sequenc A; Reference number: S01267; MUD:88121698
A; Accession: S01267; MUD:88121698
A; Rociosidues: 1-86, S', 88-102, 'L', 104-127, 'Y', 129-141, 'M', 143-187, 'R', 189-314 < SCH>A; Rosidues: 1-86, S', 88-102, 'L', 104-127, 'Y', 129-141, 'M', 143-187, 'R', 189-314 < SCH>A; Rosidues: 1-86, S', 88-102, 'L', 104-127, 'Y', 129-141, 'M', 143-187, 'R', 189-314 < SCHPS A; Rosidues: 1-801, 217, 23-37, 1991
A; Risenberger, G.; Link, T.A.; von Ahsen, U.; Waldherr, M.; Schweyen, R.J.
A; Title: MRS4, two suppressors of mtRNA splicing defects in yeast, are new m A; Reference number: S13532; MUID:91108815
A; Accession: S20228
A; Molecule type: DNA
A; Residues: 19-314 < WIE
A; Residues: 19-314 < WIE
A; Reference number: S56912
A; Accession: S56915
A; Accession: S56915
A; Residues: 1-314 < KAN>
A; Residues: 1-314 < 
                                                                                                                                                                mtRNA splice defect-suppressing mitochondrial carrier MRS3 - yeast (Saccharomyces cer N;Alternate names: protein J0675; protein YJL133w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 21-Jul-2000
C;Accession: S55179; S01267; S20228; S56915; S71664
R;Katsoulou, C; Tzermia, M; Alexandraki, D.
submitted to the EMBL Data Library, May 1995
A;Description: The complete sequence of a 40.7 kb segment located on the left arm of yeast hypothetical proteins.
A;Reference number: S55159
A;Accession: S55179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: probably involved in splicing of all intron for COB gene; essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S71664
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-314 < KARP
A; Cross-references: EMBL: X87371; NID: 9854542; PIDN: CAA60822.1; PID: 9854563
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
A; Cross-references: SGD: S0003669; MIPS: YJL133W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: mitochondrial inner membrane; mitochondrian; pre-mRNA splicing F;30-119/Domain: ADP,ATP carrier protein repeat homology <ACP1>F;27-211/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;216-311/Domain: ADP,ATP carrier protein repeat homology <ACP2>F;216-311/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.1%; Score 125.5; DB 2 27.9%; Pred. No. 5.2e-05; iive 17; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of chromosome XI.
A; Reference number: S71643; MUID:96408771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 10L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Probable

Probable

NiAlternate names: hypothetical protein [imported] - Arabidopsis thaliana

NiAlternate names: hypothetical protein T27E13.10

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001

C;Accession: T00582; C84705

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaulsubmitted to the EMBL Data Library, May 1998

A;Description: Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence.

A;Reference number: 214178

A;Accession: T00582

A;Status: translated from GB/EMBL/DDBJ

A;Residues: 1-331 <-ROUS

A;Status: translated from GB/EMBL/DDBJ

A;Residues: 1-313 <-ROUS

A;Residues: 1-313 <-ROUS

A;Residues: T31 <-ROUS

A;Experimental source: cultivar Columbia

A;Experimental source: cultivar Columbia

B;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, M.; Vanken, S.E.; Umayam, L.; Tallon, L.

B;Lin, X.; Rouls S.; Rounsley, S.D.; Shea, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487

A;Status: preliminary

A;Residues: 1331 <-ROUS

A;Status: preliminary

A;Residues: DAR

A;Res
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                          A,Cross-references: GB:AE005172; NID:g8954043; PIDN:AAF82217.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE002093; NID:g3150404; PIDN:AAC16956.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDVIHPGG--NSHIANGAAGCVATLLHDAAMNP-----AEGNDSSTYHSVGSCT- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 MOALRSCP-IKPIGIROAFRSIIKTDGPSALYRGIWAMGLGAGPAHAVYFSFYEVSKKFL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 143.5; DB 2
; Pred. No. 2.2e-06;
16; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.0%; Score 139; DB 2; 36.2%; Pred. No. 2.4e-06; Live 15; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 -----CISLQFAEESTSVLVGNSVT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 RVLREEGIGAFYASYRTTVLMNAPFT 199
                                                                                                                                                                                                                                                                                                                                                                                                            20.6%;
33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-781 <STO>
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Best Local Similarity
Matches 42; Conserv
A; Accession: A86205
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A Map position: 2
A; Introns: 82/1; 113/1; 153/2; 179/2; 259/3; 359/3
A; Introns: 82/1; 113/1; 153/2; 179/2; 259/3; 359/3
C; Superfamily: Caenorhabditis probable carrier protein c2; ADP, ATP carrier protein repeat homology #status atypical <ACP1
E; 44-43,141-193/Domain: ADP, ATP carrier protein repeat homology <ACP2>
E; 201-285/Domain: ADP, ATP carrier protein repeat homology <ACP2>
E; 201-285/Domain: ADP, ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable carrier protein c2 - Caenorhabditis elegans
C;Species: Sapple: S44092; T24753
R;Runswick, M.J.; Philippides, A.; Lauria, G.; Walker, J.E.
Submitted to the EMBL Data Library, November 1993
A;Description: Extension of the mitochondrial transport superfamily: sequences of B;Accession: S44092
A;Reference number: S44090
A;Accession: S44092
A;Acture: preliminary
A;Molecule type: mRNA
A;Residues: 1-384 <RUN>
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                                                                                                                                                                     carrier protein repeat homology
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-384 <WIL>
A;Cross-references: EMBL:Z49070; PIDN:CAA88869.1; GSPDB:GN00020; CESP:T09F3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 VLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIAN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 QPDPAARYRN-VLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKK--TLS 61
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                                 A, Cross-references: SGD:SO001760; MIPS:YKR052c
A, Map position: 11R
A; Genome: nuclear
C; Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein
C; Superfamily: ADP, ATP carrier protein repeat homology <ACPI-F:117-201/Domain: ADP, ATP carrier protein repeat homology <ACPI-F:117-201/Domain: ADP, ATP carrier protein repeat homology <ACPI-F:117-201/Domain: ADP, ATP carrier protein repeat homology <ACPI-F:206-301/Domain: ADP, ATP carrier protein repeat homology <ACPI-F:206-301/Domain: ADP, ATP carrier protein repeat homology <ACPI-F:206-301/Domain: ADP, ATP carrier protein repeat homology CACPI-F:206-301/Domain: ADP, ATP CARRIER ADP, ATP 
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.3%; Score 106; DB 2; Best Local Similarity 32.5%; Pred. No. 0.0046; Matches 25; Conservative 12; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|: | || | : | :| || || EVLIP--NSAIVHMVSAGSAGFVAA----SAVNP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 DVIHPGGNSHIAN----GAAGCVATLLHDAAMNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental source: clone T09F3
C, Genetics:
A, Gene: CESP:T09F3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 ALSGTIATIAADALMNP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 GAAGCVATLLHDAAMNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 33; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable RNA splicing proteinmitochondial carrier protein - fission yeast (Schizosacchar Cispecies: Schizosaccharomyces pombe
Cispecies: Schizosaccharomyces pombe
Cispecies: Osbec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
Cispecies: T39149
R:Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
R:Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
A:Reference number: 221748
A:Accession: T39149
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-303 < Colly
A:Residues: 1-303 < Colly
A:Cross-references: EMBL:299168; PIDN:CAB16300.1; GSPDB:GN00066; SPDB:SPAC8C9.12c
A:Experimental source: strain 972h-; cosmid c8C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Saccharomyces cerevisiae
C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jul-2000
C; Accession: 813533; 838126
R; Wiesenberger, G.; Link, T.A.; von Ahsen, U.; Waldherr, M.; Schweyen, R.J.
J. Mol. Biol. 217, 23-37, 1991
A; Title: MRS3 and MRS4, two Suppressors of mtRNA splicing defects in yeast, are new memb
A; Reference number: 813532; MUID:91108815
A; Accession: 813533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mtRNA splice defect-suppressing mitochondrial carrier MRS4 – yeast (Saccharomyces cerevi
N;Alternate names: protein YKR052c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: SPDB:SPAC8C9.12c
A;Map position: 1
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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                                                                                                                               72 KNMLSQISHISTSEGTLALWKGVQSVILGAGPAHAVYFGTYEFCKKNLIDSSDTQTHHPF 131
                                                                                    ---YHSVGSCTC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 NGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSCTCISLQFAEESTSVLVGNSVT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 NVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-304 <VIS>
A;Residues: 1-304 <VIS>
A;Cross-references: EMBL:228277; NID:g486506; PID:g486507; MIPS:YKR052c
A;Experimental source: strain S288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA39828.1; PID:93996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Indels
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March 1994
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Pred. No. 0.00022;
1; Mismatches 48
                                                                        73 ANGAAGCVATLLHDAAMNPAEG-----NDSST---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X56444; NID:g3995;
R;ViSsers, S.; Urrestarazu, L.A.; Jauniaux,
submitted to the Protein Sequence Database,
A;Reference number: S38118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                         109 ISLQFA-----EESTSVL 121
                                                                                                                                                                                                                                                                                                                     192 MNIPFAAFNFVIYESSTKFL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 17.1%;
1 Similarity 27.6%;
34; Conservative 2
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Best Local Similarity
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A; Residues: 1-304 <JMO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 AFY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
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hypothetical protein At2g22500 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C.Accession: D84613
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-788, 1999
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487
Rigalisson, F.; Dujon, B.
Yeast 12, 877-885, 1996
A;Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome A;Reference number: S71713; MUID:96437977
A;Reference number: S71724
                                                                                                                                                                                                  A Molecule type: DNA
A; Residues: 1-307 <GAW>
A; Residues: 1-307 <GAW>
A; Residues: 1-307 <GAW>
A; Cross-references: EMBL:X92441; NID:g1050762; PIDN:CAA63185.1; PID:g1050774
C; Genetics:
A; Map position: 15R
A; Map position: 15R
A; Note: YOR222*
C; Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C; Keywords: duplication; mitochondrion; transmembrane protein
F; 9-107/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F; 115.201/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F; 208-300/Domain: ADP,ATP carrier protein repeat homology <ACP2>
C; 208-3
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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hypothetical protein DKF2p434C119.1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T43493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 RYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNS 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.7%; Score 95; DB 2; Length 307; Best Local Similarity 27.7%; Pred. No. 0.059; Matches 23; Conservative 17; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;; Score 94.5; DB 2; Length 3;; Pred. No. 0.068; 23; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 THVSASFAAGFVASV----ASNPVD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 SHI-ANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 HIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.6%;
31.8%;
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A; Residues: 1-313 <STO>
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                                                                                                                                                                                          Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Hughes, B.; Hitzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowartz, J.R.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
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N;Alternate names: protein 05064; protein YOR222w; protein YOR50-12
C;Species: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
C;Accession: 860949; 867115; B37984; 871724
R;Galisson, F.; Dujon, B.
Submitted to the EMBL Data Library, October 1995
A;Bescription: Sequence and analysis of a 33 kb fragment from the right arm of chromosom A;Reference number: 860938
A;Accession: 860949
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A; Residues: 1-307 <GAL>
A; Cross-references: EMBL:X92441; NID:g1050762; PID:g1050774
A; Cross-references: EMBL:X92441; NID:g1050762; PID:g1050774
Byoyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Michaux, G.; Thierry, A.; Dujon, submitted to the Protein Sequence Database, July 1996
A; Reference number: S67104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE005173; NID:g6453859; PIDN:AAF09043.1; GSPDB:GN00141
C;Genetics:
    hypothetical protein F19K16.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96830
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J. Biol. Chem. 265, 19736-19741, 1990
A;Title: Mitochondrial phosphate transport. N-ethylmaleimide insensitivity
A;Reference number: A37984; MUID:91060585
A;Accession: B37984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 ANGAAG-----CVATLLHDAAMNPAEGNDSSTYHSVGSCTCISLQFAEESTSVL---VG 123
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A;Residues: 1-307 <BOY>
A;Cross-references: EMBL:275130; NID:g1420513; PID:g1420514; MIPS:YOR222w
A;Experimental source: strain $288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
0.057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 95; DB : Fred. No. 0.05; 17; Mismatches
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28.5%;
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Best Local Similarity 28.58
Matches 35; Conservative
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A; Residues: 1-296 <STO>
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: G86583
A; Accession: G86583
A; Status: preliminary
A; Model of the plant Arabidopsis.
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N.Alternate names: protein T21J18.120
C.Specias Arabidopsis thaliana (mouse-ear cress)
C.Jate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
C.Accession: T49281
R.Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, submitted to the Protein Sequence Database, April 2000
A.Reference number: Z25021
A.Accession: T49281
A.Accession: T492
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A;Introns: 96/3; 232/1; 303/3; 345/2
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005172; NID:910092331; PIDN:AAG12742.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 TLSDVIHPG-----GNSHIANGAAGCVATLL--HDA----AMNPAEGNDSSTYHSVGS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 QSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL--NVTATGAGPAH-ALYFACYEKLKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.9%; Score 90; DB 2; 28.9%; Pred. No. 0.23; tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%; Score 90; DB 2, ilarity 27.5%; Pred. No. 0.19; Conservative 26; Mismatches
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Best Local Similarity 28.9%
Matches 28; Conservative
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C; Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 CTCISLOFAEE 116
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Best Local Similarity
Matches 36; Conserv
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C. Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Sep-1999
C. Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Sep-1999
C. Accession: J04459
R. Sullivan, T.D.; Strelow, L.I.; Illingworth, C.A.; Phillips, R.L.; Nelson Jr., O.E. Plant Cell 3, 1337-1348, 1991
A. Title: Analysis of maize brittle-1 alleles and a defective suppressor-mutator-induced A; Reference number: J01459; MUID:93005685
A. Accession: J01459
A. Molecule type: mRNA
A; Reference number: J01459; MUID:9168425; PIDN:AAA33438.1; PID:9168426
A; Comment: This protein acts as an adenylate translocator in amyloplasts.
C. Comment: This protein acts as an adenylate translocator in amyloplasts.
C. Comment: This protein acts as an adenylate translocator in amyloplasts.
C. Comment: This protein acts as an adenylate translocator in amyloplasts.
C. Superfamily: Btl protein; ADP,ATP carrier protein repeat homology
C. Keywords: Chloroplast; duplication; transmembrane protein repeat homology ACPP>
F. 137/Domain: transmembrane #status predicted <AMT>
F. 137/Domain: transmembrane #status predicted <AMI>
F. 220-247/Domain: ADP,ATP carrier protein repeat homology ACPP>
F. 229-247/Domain: transmembrane #status predicted <AMI>
F. 323-413/Domain: transmembrane #status predicted <AMI>
F. 323-413/Domain: transmembrane #status predicted <AMI>
F. 323-413/Domain: transmembrane #status predicted <AMI>
F. 327-347/Domain: transmembrane #status predicted <AMI>

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTL--- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 ALTSDLYAP------MVAGALARLGTVTVISPLEIMRTKLQAQHVSYRELGAC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
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R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, December 1999
A:Reference number: 222516
A:Accession: T43493
A:Molecule type: mRNA
A:Residues: 1-351 < AAA>
A:Cross-references: EMBL:AL133584
A:Cross-references: EMBL:AL133584
A:Rosidues: source: adult testis; clone DKFZp434C119
C;Genetics:
A:Note: DKFZp434C119.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.6%; Score 94.5; DB 2; Length 35:
Best Local Similarity 29.6%; Pred. No. 0.077;
Matches 34; Conservative 15; Mismatches 39; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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hypothetical protein C54G10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2029
R;Matthews, L.
Submitted to the EMBL Data Library, June 1996
A;Reference number: Z19240
A;Reference number: Z19240
A;Refatus: pre-Liminary; translated from GB/EMBL/DDBJ
A;Retus: pre-Liminary; translated from GB/EMBL/DDBJ
A;Residues: 1-310 <WIL>
A;Residues: 1-310 <WIL>
A;Residues: 1-310 <WIL>
A;Genetics: Clone C54G10
C;Genetics: Cone C54G10
C;Genetics: A;Genetics: A;Genetics: Clone C54G10
C;Genetics: A;Genetics: Clone C54G10
C;Genetics: Cspecifion: S
A;Introns: 14/1; 63/1; 155/2; 256/2; 299/3
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LQPDPA-ARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKK---- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
12.8%; Score 89; DB 2; Length 310;
Best Local Similarity 25.5%; Pred. No. 0.24;
Matches 39; Conservative 21; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : | | : | | 234 IKQTYLERGYRGFFVGLNSALIRAFPSNAATFF 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 ISLQFAEES-----TSVLV----GNSVTLF 129
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Search completed: August 27, 2002, 03:57:45 Job time: 4951 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 27, 2002, 04:16:49 Run on:

/ Search time 37.5 Seconds
(without alignments)
135.260 Million cell updates/sec

Title:

US-09-870-113-12 695 1 MQSLQPDPAARYRNVLEALW......QFAEESTSVLVGNSVTLFYH 131 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched: 105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P10566 saccharomyc	P23500 saccharomyc	7 sacch	Q9bzj4 homo sapien	zea n	Q9hc21 homo sapien				Q01952 synechocyst				_	Q02978 homo sapien	Q09461 caenorhabdi		P00320 cyanophora		Q27238 anopheles g	Q9cr62 mus musculu	Q03829 saccharomyc				P28556 aglaothamni	P80557 anabaena sp			spir		anaba	Q9ubx3 homo sapien
SUMMARIES	ID	MRS3_YEAST	MRS4_YEAST	ODC2_YEAST	CG69_HUMAN	BT1_MAIZE	DNC_HUMAN	PHAB_CYACA	PHAB_GALSU	SFC1_YEAST	PHAB_SYNY3	PHAB_SYNY4	PHAB_FREDI	M2OM_BOVIN	PHAB_MASLA	M2OM_HUMAN	YQ51_CAEEL	GGH_RAT	PHAB_CYAPA	YG5F_YEAST	ADT_ANOGA	M2OM_MOUSE	YM39_YEAST	PHAB_SYNEL	PUTA_SALTY	SA18_HUMAN	PHAB_AGLNE	PHAB_ANASP	PHAB_ANAVA	PHAB_SYNP6	PHAB_SPIPL	UCP2_PIG	PHAB_ANACY	DIC_HUMAN
	DB	•	7	~	П	П	П	П	П	٦	Ч	٦	Н	Н	-	~	Н	Н	Н	Н	Н	Н	Н	Н	-	Н	Н	-	Н	-	-	-	7	-
	Query Match Length DB		304	307	359	436	320	161	161	322	161	161	162	313	161	313	328	317	161	366	301	313	368	161	1320	315	161	161	161	161	161	309	161	287
dP	Query Match	18	5.	13.7	13.6	13.4	12.9	12.9	12.4	\sim	11.9	11.9	11.6	11.6	11.4	11.4	11.4	11.4	11.3	11.2	11.2	11.2	11.1	11.0	11.0	10.9	10.9	10.9	10.9	10.9	10.7		10.6	10.6
	Score	125.5	106	95	94.5	93	90	89.5	86.5	86.5	82.5	82.5	80.5	80.5	79.5	79.5	79.5	79	78.5	78	77.5	77.5	77	76.5	76.5	92	75.5	75.5	75.5	S	74.5	\sim	73.5	73.5
	Result No.	н	7	ო	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

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Q9qzd8 mus musculu p97700 rattus norv Q9db41 mus musculu Q9va73 drosophila Q9h2d1 homo sapien P56499 rattus norv O52326 salmonella Q59752 rhizobium m P27080 chlamydomo Q12375 saccharomyc P38152 saccharomyc O52485 klebsiella
DIC_MOUSE MACOM_RAT SA18_MOUSE CMC1_DROME MET_HUMAN UCP3_RAT YEBH_SALTY FPG_RHIME ADT_CHIRE ORT1_YEBAST TXTP_YEBAST PUTA_KLEAE
287 313 312 315 695 315 308 299 301 292 292 299
01100100000000000000000000000000000000
73.5 73.5 73.5 71.5 71.5 70 70 69.5 69.5
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

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inner membrane
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Q99297;
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TRANSMEM
SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vissers S., Urrestarazu L.A., Jauniaux J.-C.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MRS4 SUPPRESSES A MITOCHONDRIAL SPLICE DEFECT IN THE FIRST INTRON OF THE COB GENE. IT MAY ACT AS A CARRIER, EXERTING ITS SUPPRESSOR ACTIVITY VIA WOULLATION OF SOLUTE CONCENTRATIONS IN THE MITOCHONDRION (POSSIBLY OF CATIONS). NOT ESSENTIAL.
-!- SWBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                         72 KNMLSQISHISTSEGTLALWKGVQSVILGAGPAHAVYFGTYEFCKKNLIDSSDTQTHHPF 131
                                                                                                                                                                                                                                                                                                                                                                          Wiesenberger G., Link T.A., von Ahsen U., Waldherr M., Schweyen R.J.; "MRS3 and MRS4, two suppressors of mtRNA splicing defects in yeast, are new members of the mitochondrial carrier family."; J. Mol. Biol. 217:23-37(1991).
                                                                                                                                                                                                                                                                                                                                                             73 ANGAAGCVATLLHDAAMNPAEG-----NDSST------YHSVGSCTC 108
                                                                                                                                                                                                                                                                          ; Score 125.5; DB 1; Length 314;
; Pred. No. 5e-06;
17; Mismatches 53; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                   13 RNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHI 72
                                                                                           InterPro; IPR001993; Mitoch_carrier.
Pfam: PF00153; Mito_carr; 3.
PROSITE: PS00215; MITOCH_CARRIER; 2.
Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                           861145CE6E4EF321 CRC64;
                                                                                                                                            BLOCK I (APPROXIMATE).
BLOCK II (APPROXIMATE).
BLOCK III (APPROXIMATE)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrial RNA splicing protein MSR4. MRS4 OR YKR052C.
                                                                                                                                                                                         POTENTIAL. POTENTIAL.
                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                    POTENTIAL
         EMBL; X56445; CAA39829.1; -.
EMBL; X56445; CAA39830.1; ALT_INIT.
EMBL; X06239; CAA29582.1; ALT_SEQ.
EMBL; X07371; CAA60822.1; -.
EMBL; X49408; CAA89428.1; -.
PIR; S01267; S01267.
PIR; S20228; S20228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91108815; PubMed-1703236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                     109 ISLQFA-----EESTSVL 121
                                                                                                                                                                                                                                                                                                                                                                                                                    18.1%;
27.9%;
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                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                               285 ;
314 AA;
                                                                                  S0003669; MRS3
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 39; Conserv
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SEQUENCE FROM N.A.
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01-NOV-1991 (Rel.
15-DEC-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                     MRNA processing.
REPEAT 121
REPEAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-M1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRS4_YEAST
P23500;
                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
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MRS4_YEAST
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 MISQISKISTWEGSWALWKGVQSVILGAGPAHAVYFGTYEFCKARLISPEDMQTHQPMKT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. STRONG, TO YEAST MRS3; BOTH PROTEINS MAY BE ISOFORMS OF THE SAME CARRIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 VLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIAN 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHĀRACTERIZATION.
PubMed-11013234;
Balmieri L., Agrimi G., Runswick M.J., Fearnley I.M., Palmieri F.,
Walker J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Galisson F., Dujon B.; "Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV of the yeast Saccharomyces cerevisiae."; Yeast 12:877-885(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5ABBF9858B547EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOCK II (APPROXIMATE).
BLOCK III (APPROXIMATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 106; DB 1; 32.5%; Pred. No. 0.00057; ive 12; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-Chondrial 2-oxodicarboxylate carrier 2.
0DC2 OR YOR222W OR YOR50-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 AA
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                                                                                                                                                                                                                                                                                                                                          PIR; S13533; S13533.
SGD; S0001760; MRS4.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
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MEDLINE-96437977; PubMed-8840505;
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Best Local Similarity 32.54
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1110
202
304
41
102
139
139
228
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304 AA;
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203
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83
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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      RREAR BRANCH BRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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   "Identification in Saccharomyces cerevisiae of two isoforms of a novel
                                                                                    membranes of mitochondria. Can transport 2-oxoadipate, 2-oxoadipate, 2-oxoadirante, adipate, glutarate, 2-oxoadipate, 2-oxoadipate, 2-oxoadipate, oxaloadise, oxaloadise, citrate and malate. The main physiological role is probably to supply 2-oxoadipate and 2-oxoglutarate from the mitochondrial matrix to the cytosol where they are used in the blosynthesis of lysine and glutamate, respectively, and in lysine catabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 RYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Overexpression of the human 2-oxoglutarate carrier lowers mitochondrial membrane potential in HEK-293 cells: contrast with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu X.X., Lewin D.A., Zhong A., Brush J., Schow P.W., Sherwood S.W.,
Pan G., Adams S.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG69_HUMAN STANDARD, PRT; 359 AA.
CG69_HUMAN STANDARD, O9P182;
01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
Mixochondial carrier protein CGI-69 (PR02163).
Mixochondial carrier protein CGI-69 (PR02163).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vorrebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; iraccinity Pfam; Professional Professional Professional Prints, PR009246; MITOCHCARNIER, 3. PROSITE; PS00215; MITOCH_CARRIER; 3. MItochondrion; Inner membrane; PoTENPIAL. Transmembrane; Transport. POTENTAL.
                              mitochondrial transporter for 2-oxoadipate and 2-oxoglutarate."; J. B401. Chem. 276:1916-1922(2011).
-i-FUNCTION: Transports C5-C7 oxodicarboxylates across the inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SUBCELLULAR LOCATION, AND
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                                                                                                                                                                                                                                                                                                                                                                                       -!- DOMAIN: COMPOSED OF THREE HOWOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match . 13.7%; Score 95; DB 1; Length 307; Local Similarity 27.7%; Pred. No. 0.0085; nes 23; Conservative 17; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4089082A64DBA97C CRC64;
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 QKISIAAGASAGMTEAAVIVPFE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 HIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 AA; 34007 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z75130; CAA99440.1; -. EMBL; X92441; CAA63185.1; -.
                                                                                                                                                                                                                                                                                                                                                                   inner membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/CGI-69L (shown here) and 2; are produced by alternative splicing.
-1- TISSUE SPECIFICITY: Expressed in many tissues. Abundant in testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S
Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
NuBob human cDMA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by analysis of cDNA clones from human fetal liver.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21154917; PubMed=11230166; Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Mansorge W., Boecher M., Bloceker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
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Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
Alternative splicing; Polymorphism.
                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
Identification of novel human genes evolutionarily conserved Caenorhabditis elegans by comparative proteomics.";
Genome Res. 10:703-713(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and kidney.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
unique cold-induced mitochondrial carrier CGI-69.";
Biochem. J. 353:369-375(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 15-359 FROM N.A. (ISOFORM 1). TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1). TISSUE=Brain, and Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 11:422-435(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Testis;
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9600C05F603E9DAE CRC64;

46627 MW;

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EMBL; AJ251857; CAC27560.1; -.
 436 AA;
                                                                                                                                                                                                                                                                                                                       rissue=Liver
                                                                                                                                                         DNC_HUMAN
                                                                                                                                                                                                                              protein 1)
SEQUENCE
                                  Query Match
Best Local 9
                                                        Matches
                                                                                                                                             DNC HUMAN
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                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                      100 DP-TRFTGTMDAFVKIVRHEGTRTLW---SGLPATLVMTVPATAIYFTAYDQLKAFLCGR 155
                                                                                                                                                          Gaps
                                                                                                                                                                                 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTL--- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Analysis of maize brittle-1 alleles and a defective
Suppressor-mutator-induced mutable allele.";
Plant Cell 3:1337-1348(1991).
-!- FUNCTION: COULD PLAY A ROLE IN AMYLOPLAST MEMBRANE TRANSPORT.
                                                                                                                                                                                                                                             156 ALTSDLYAP------MVAGALARLGTVTVISPLELMRTKLQAQHVSYRELGAC 202
                                                                                                                                                                                                                              ---SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSC 106
                                                                                                                                                         39; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93005685; PubMed-1668652;
Sullivan T.D., Strelow L.I., Illingworth C.A., Phillips R.L.,
Nelson O.E. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
-i- TISSUE SPECIFICITY: ENDOSPERM OF DEVELOPING KERNELS.
-i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                    Score 94.5; DB 1; Length 359; Pred. No. 0.012;
                                                        LPSSLQSTG -> W (IN ISOFORM 2).
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Interpro; IPR0012067; Mit_carrier.
Interpro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCARRIER.
ITANSIT peptide; Chloroplast; Amyloplast; Transmembrane.
TRANSIT 175 BBITTLE-1 PROTEIN.
CHAIN 76 436 BBITTLE-1 PROTEIN.
                                                                                         G -> R (IN REF. 6).
952AA3DB5F5F9BD1 CRC64;
                                                                            /FTId=VAR_012756
                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Brittle-1 protein, chloroplast precursor.
                                                                                                                                              ; Pred. No. 0.01;
15; Mismatches
                                                                                                                                                                                                                                                                                                             436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                      POTENTIAL. POTENTIAL.
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  POTENTIAL
                                                                                                    39214 MW;
                                                                                                                                    13.6%;
29.6%;
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                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                           STANDARD;
 142
1181
235
279
338
72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JQ1459; JQ1459.
                                                                                        266
359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                        mays (Maize)
 122
161
215
259
318
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229
327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MaizeDB; 47578;
                                                                                                                                 Query Match
Best Local Simi
Matches 34;
                                                                                                                                                                                                                                                                                                          BT1_MAIZE
P29518;
           TRANSMEM
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TRANSMEM
                                                                                                   SEQUENCE
                                            PRANSMEM
                                                      VARSPLIC
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                                                                   VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Lung;
Straubberg R.;
Straubberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Responsible for the uptake of deoxynucleotides into the matrix of the mitochondria. Transports all four deoxy NDPS, and, less efficiently, the corresponding dNTPs. Does not transport dNMPS, NMPS, MAPS, deoxynucleosides, nucleosides, purines, or pyrimidines. Supply deoxynucleotides to the mitochondrial matrix for conversion to triphosphates and incorporation into mitochondrial DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
DISEASE: Likely to be medically important by providing the means of uptake into mitochondria of nucleoside analogs, leading to the mitochondrial impairment that underlies the toxic side effects of such drugs in the treatment of viral illnesses, including AIDS,
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dolce V., Fiermonte G., Runswick M.J., Palmieri F., Walker J.E.; "The human mitochondrial deoxynucleotide carrier and its role in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: Expressed in all tissues examined except for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  placenta. Highest levels in colon, kidney, lung, testis, spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrial deoxynucleotide carrier (Mitochondrial uncoupling
                                                                             ;
0
                                                                                                                                                                                                        |:||| |:: |:: || || || 365 YQNVLHAIYCILKKEGAGGLYRGLGPSCIKLMPAAGIAFMCYEACKKILVD 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY
                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and in cancer therapy.
SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
    DB 1; Length 436;
                                                                                                                                                           12 YRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSD
                                                                             23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Renard S., Mondesert G., Besnard F.;
"MUP 1, a mitochondrial uncoupling protein.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 98:2284-2288(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                        Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                          320 AA
                                                                             7; Mismatches
13.4%; Score 93; 41.2%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toxicity of nucleoside antivirals.
                                                                                 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLC25A19 OR DNC OR MUP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inner membrane.
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Galdieria sulphuraria.
                                                                                                       161 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                PHAB_GALSU
                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast.
Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
                                                                                                                                                                                                                                                                                                                             54 DPSAKYHGILQASRQILQEEGPTAFWKGHVPAQILSIGYGAVQFLSF-----EMLTEL 106
                                                                                                                                                                                                                                                                                                                                                                   64 IHPGG-----NSH-IANGAAGCVATLLHDAAMNP-----AEGND---SSTYHSV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM THE PHYCOBILIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM ABSORPTION AT APPROXIMATELY 650 NANOMEPERS.
-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- PTM: CONTAINS ONE COVALENTLY LINKED BILLIN CHROMOPHORE.
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                     7 DPAARYRNVLEALWRIIRTEG---LWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Mol. Evol. 51:382-390(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gloeckner G., Rosenthal A., Valentin K.; "The structure and gene repertoire of an ancient red algal plastid
                                                                                                                 PROSITE; PS00215; MITOCH_CARRIER; 1.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
TRANSMEM 19 39 POTENTIAL.
                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                    Length 320;
                                                                                                                                                                                                                                                                           33; Indels
                                                                                                                                                                                              POTENTIAL.
57CE0F01D538B1BE CRC64;
                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-ocr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
16-ocr-2001 (Rel. 40, Last annotation update)
Allophycocyanin beta chain.
                                                                                                                                                                                                                                                             0.031;
                                                                                                                                                                                                                                             161 AA
                                                                                                                                                          POTENTIAL. POTENTIAL.
                                                                                                                                                                                    POTENTIAL
                                                                InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20496959; PubMed-11040290;
                                                                            InterPro, IPR002067; Mit_carrier. Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER.
AJ301616; CAC37793.1; -. AF182404; AAG16903.1; -. BC001075; AAH01075.1; -.
                                       BC005120; AAH05120.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF022186; AAF12903.1; -.
                                                                                                                                                                                                            35511 MW;
                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                      142
193
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87
122
173
173
320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyanidium caldarium.
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-2771;
                                                   606521;
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163 GT 164
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Q9TLS8;
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TRANSMEM
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                                                                                                                                                          TRANSMEM
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Chloroplast.
Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
Galdieria.
                                                                                                                                                                                                                                                                                                                                           63 VIHPGGNSHIANGAAGCVATL---LHDAAMNPAEGNDS-----STYHSVG---S 105
                                                                                                                                                                                                                                                                                                                                                                   rhodophyte, Cyanidium caldarium. The complete amino acid sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kostrzewa M., Zetsche K.;
"Organization of plastid-encoded ATPase genes and flanking regions including homologues of infB and tsf in the thermophilic red alga galdieria sulphuraria.";
Plant Mol. Biol. 23:67-76(1993).
Plant Mol. Biol. 23:67-76(1993).
FROM THE PHYCOBILIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                       7 DPAARY--RNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL--SD 62
                                                                                                                                                                                                                                                                                                         13 DVOGKYLDNNSIEKLRSYFQT-GELRVRAAASISANAAG-----IIKEAVAKSLLYSD
HSSP; P00318; 1B33.
InterPro; IRRO01659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
Mchylation; Chloroplast.
METHYLATION (BY SIMILARITY).
BINDING 81 81 PHYCOCYANOBILIN CHROMOPHORE (BY
                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                12.9%; Score 89.5; DB 1; Length 161; 28.3%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu B., Troxler R.F.; "A Cyanidium caldarium allophycocyanin beta subunit gene."; Plant Physiol. 103:293-294(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Offner G.D., Troxler R.F.; Primary structure of allophycocyanin from the unicellular
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=14-1-1 / ISOLATE 107.79/GOETTINGEN; KOSTIZEWA M., Zetsche K.; Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                             SIMILARITY).
3AFF46A2162AFDFA CRC64;
                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 30, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 AA
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 51-161 FROM N.A.
STRAIN=14-1-1 / ISOLATE 107.79/GOETTINGEN;
MEDLINE-94033298; PubMed-8219057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the alpha and beta subunits.";
J. Biol. Chem. 258:9931-9940(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=83290919; PubMed=6885776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94269195; PubMed-8208852;
                                                                                                                                                                                                                                    18;
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21-JUL-1986 (Rel. 01, Created)
01-OCT-1994 (Rel. 30, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                              17471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  106 CTCISLQFAEESTSVLVG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                          Allophycocyanin beta chain.
                                                                                                                                                                                                  Query Match 12.9°
Best Local Similarity 28.3°
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Ramezani Rad M., Kirchrath L., Hollenberg C.P.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
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       RRARRER RRARRE
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 IANGAAGCVATL---LHDAAMNPAEGNDS------STYHSVG---SCTCISLQFA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 TTRRYAACIRDLDYYLRYATYSMLAGDPSILDERVLNGLKETYNSLGVPIGATIQSIQAM 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 NVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL--SDVIHPGGNSH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 SIIEKLKGYFQT-GELRVRAAATIAANAAG-----IIKDAVAKSLLYSDITRPGGNMY 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-94201187; Pubmed-7908717;
Fernandez M., Fernandez E., Rodicio R.;
**RARI, a gene encoding a protein related to mitochondrial carriers, is essential for acetyl-CoA synthetase activity in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Electron transport; Photosynthesis; Bile pigment; Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBL_FaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.4%; Score 86.5; DB 1; Length 161; Best Local Similarity 27.7%; Pred. No. 0.032; Matches 36; Conservative 18; Mismatches 49; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHYLATION (BY SIMILARITY).
PHYCOCYANOBILIN CHROMOPHORE.
I -> S (IN REF. 2).
I -> R (IN REF. 3).
GN -> LD (IN REF. 3).
Y -> L (IN REF. 3).
S -> P (IN REF. 3).
S -> P (IN REF. 3).
W, E6957PEH49370BA8 CRC64;
ABSORPTION AT APPROXIMATELY 650 NANOMETERS. SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 32, Last sequence update) (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001659; Phycobilisome. Pfam; PF00502; Phycobilisome; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthetase activity).
SFC1 OR ACR1 OR YJR095W OR J1921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 S
17433 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                   EMBL; L12540; AAB01577.1; -. EMBL; X74548; CAA52642.1; -.
                                                                                                                                                                                                                                                                                                                                                       EMBL; X66698; CAA47243.1; -.
                                                                                                                                                                                                                                                                                                                                                                              PIR; A00330; AFKKB.
PIR; S37090; S37090.
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134 KEVTSSLVGS 143
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SEQUENÇE FROM N.A.
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01-MAR-2002
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P33303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isocitrate by the action of isocitrate lyase in the cytosol, into the mitochondrial matrix in exchange for fumarate.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial.
-!- INDUCTION: BY ETHANOL OR ACETATE AS SOLE CARBON SOURCES. REPRESSED BY GLUCOSE.
                                                                                           "Identification of the yeast ACR1 gene product as a succinate-fumarate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 EPNAGPKYNNAIHAAYTIVKEEGVSALYRGVSLTAARQATNQGANFTVYSKLKEFLQNYH 207
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                      MEDLINE-98055465; PubMed-9395087;
Palmieri L., Lasorsa F.M., De Palma A., Palmieri F., Runswick M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
MEDLINE=93054612; PubMed=1429645;
MEDLINE=93054612; PubMed=1429645;
Su X., Goodman P., Bogorad L.;
"Excitation energy transfer from phycocyanin to chlorophyll in an apcA-defective mutant of Synechocystis sp. PCC 6803.";
J. Biol. Chem. 267:22944-22950(1992).
                                                                                                                  transporter essential for growth on ethanol or acetate."; FEBS Lett. 417:114-118(1997).
                                                                                                                                                                                                                                                                                                               -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 322;
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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Last annotation update)
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(Rel. 40, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z25485; CAA80973.1; -. EMBL; Z49595; CAA89624.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S36407; S36407,
PIR; S43280; S43280,
SGD; S0003856; SFC1.
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CHARACTERIZATION.
MEDLINE=98055465;
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                                   MEDLINE=93222481; PubMed=8467079;
Dimagno L.M., Haselkorn R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17242 MW;
                                                                                                                                                                                                                                                                                                                                                                            EMBL; L02308; AAA69683.1; -.
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                    SEQUENCE FROM N.A.
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P16571:
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-1- SUBBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

-1- PIM: CONTAINS ONE COVALENTLY LINKED BILLIN CHROMOPHORE.
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                               MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K.,
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
Yasuda M., Tabata S.;
Yamada M., Yasuda M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCG6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                    Sazuka T., Ohara O.; "Towards a proteome project of cyanobacterium Synechocystis sp. strain PCC6803: linking 130 protein spots with their respective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
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63F01E5903BA1B83 CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1147;
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Mismatches
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                                                                                                                                                                                                                                                                                                                        genes.";
Electrophoresis 18:1252-1258(1997)
                                                                                                                                                                                                                                                   MEDLINE-97443974; PubMed-9298645;
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B44462; B44462.
[2]
SEQUENCE FROM N.A.
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SEQUENCE OF 1-20.
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HSSP; P00318;
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Q02924;
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PHAB_SYNY4
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"Isolation and characterization of the genes encoding allophycocyanin
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                                                                                                                                                      FROM THE PHYCOBILIPROTEIN COMPLEX, ALLOPHYCOCYANIN HAS A MAXIMUM ASSORPHION AT APPROXIMATELY 650 NANOMETERS.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
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-!- SUBBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- PIM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
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                                    subunits and two linker proteins from Synechocystis 6714.";
Plant Mol. Biol. 21:835-846(1993).
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J. Bacteriol. 170:5512-5521(1988).
-!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
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Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Fremyella.
NCBI_TaxID=1197;
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MEDLINE=89053869; PubMed=2461358;
Houmard J., Capuano V., Coursin T., Tandeau de Marsac N.;
Hognes encoding core components of the phycobilisome in the
cyanobacterium Calothrix sp. strain PCC 7601: occurrence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHYCOCYANOBILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63F0047008630A73 CRC64;
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01-AUG-1990 (Rel. 15, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 EKLKKTL--SDVIHPGGNSHIANGAAGCV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 GNDSSTYHSVG---SCTCISLQFAEESTSVLVG 123
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-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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PHAB_MASLA
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        use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                      4;
 There are no restrictions on
                                                                                                                                                                                                                                                                                                                                       55 EAVAKSLLYSDVTRPGGNMYTTRRYAACIRDLDYYLRYATYAMLAGDPSILDERVLNGLK 114
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                             54 EKLKKTL--SDVIHPGGNSHIANGAAGCVATL---LHDAAMNPAEGNDS------ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence of the bovine 2-oxoglutarate/malate carrier protein: structural relationship to other mitochondrial transport proteins."; Blochemistry 29:11033-11040(1990).

Biochemistry 29:11033-11040(1990).

Biochemistry 29:11033-11040(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN GLUCONEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INNER MITOCHONDRIAL MEMBRANE IN AN ELECTRONEUTRAL EXCHANGE FOR MALATE OR OTHER DICARBOXILIC ACIDS, AND PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PROCESSES, INCLUDING THE MALATE-ASPARTATE SHUTTLE, THE ACIDITARATE SHUTTLE, IN GLUCONEOGENESI FROM LACTATE, AND IN NITROGEN METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

BEDLINE-39091249, PubMed-1457818;

Iacobazzi V., Palmieri F., Runswick M.J., Walker J.E.;

Sequences of the human and bovine genes for the mitochondrial 2-
                                                                                                                                   InterPro; IPR001659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                          11.6%; Score 80.5; DB 1; Length 162; 32.2%; Pred. No. 0.14; Live 12; Mismatches 30; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHYLATION (BY SIMILARITY).
PHYCOCYANOBILIN CHROMOPHORE.
CAFC4C1909A3A201 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Runswick M.J., Walker J.E., Bisaccia F., Iacobazzi V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: HEART, 'LIVER, AND BRAIN. DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                               115 ETYNSLGVPVSSTVQAIQAIKEVTASLVGS 144
                                                                                                                                                                                                                                                                                                                                                                 STYHSVG---SCTCISLQFAEESTSVLVGN 124
 European Bioinformatics Institute.
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                                                                                                                                                                                         72 ME
82 PH
17268 MW;
                                                                               EMBL; M20806; AAA24875.1; -.
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 32.2%.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
82
162 AA;
                                                                                                          PIR; B30764; B30764
                                                                                               PIR; C31385; C31385
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                                                                                                                         HSSP; P00318; 1B33
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                                                                                                                                                                              Methylation.
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                                                                                                                                                                                         MOD_RES
BINDING
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sidler W., Gysi J., Isker E., Zuber H.;
"The complete amino acid sequence of both subunits of allophycocyanin, a light harvesting protein-pigment complex from the cyanobacterium Mastigocladus laminosus.";
Hoppe-Seyler's Z. Physiol. Chem. 362:611-628(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; Mito_carr; 3.
PROSITE; PS00215; MITOCH CARRIER; 2.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
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Bacteria; Cyanobacteria; Stigonematales; Fischerella.
NCBL_TaxID=1191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.6%; Score 80.5; DB 1;
30.0%; Pred. No. 0.31;
Live 15; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-FFB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Allophycocyanin beta chain.
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                                                                                                                                                                                                                                                                                                                            EMBL; X66115; CAA46906.1; -. EMBL; M58703; AAA30671.1; -. EMBL; M60662; AAA30672.1; -.
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nes 27; Conservative
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208
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PIR; S29597; S29597
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                    Ruembeli R., Suter F., Wirth M., Sidler W., Zuber H.; "Gamma-N-methylasparagine in phycobiliproteins from the cyanobacteria Mastigocladus laminosus and Calothrix.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 EAVAKSLLYSDITRPGGNMYTTRRYAACIRDLDYYLRYATYAMLAGDPSILDERVLNGLK 113
                                                                                                                                                                                                                                                                                   phycobilisomes of Mastigocladus laminosus.";
Proc. Natl. Acad. Sci. U.S.A. 96:1363-1368(1999).
-!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
FROM THE PHYCOBILIPROTEIN COMPLEX. ALLOPHYCOCYANIN HAS A MAXIMUM
ABSORPTION AT APPROXIMATELY 650 NANOMETERS.
-!- SUBJUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- SUBJUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                           Reuter W., Wiegand G., Huber R., Than M.E.;
"Structural analysis at 2.2 A of orthorhombic crystals presents the
asymmetry of the allophycocyanin-linker complex, AP.LC7.8, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
Www, Gibs.R.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 EKLKKTL--SDVIHPGGNSHIANGAAGCVATL---LHDAAMNPAEGNDS-----
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-93091249; PubMed-1457818;
Iacobazzi V., Palmieri F., Runswick M.J., Walker J.E.;
"Sequences of the human and bovine genes for the mitochondrial 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB: 1B33, 23 FEB-99.
InterPro; IPR001659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
Phycobilisome: Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.4%; Score 79.5; DB 1; Length 161; 31.5%; Pred. No. 0.18; ive 12; Mismatches 30; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rel. 41, Last sequence update)
Rel. 41, Last annotation update)
2-oxoglutarate/malate carrier protein (OGCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHYCOCYANOBILIN CHROMOPHORE.

SL -> KT (IN REF. 1).

R -> L (IN REF. 1).

N -> D (IN REF. 1).

1877DD78D7178350 CRC64;
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                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
SEQUENCE OF 55-82, AND METHYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                STRAIN-PCC 7603;
MEDLINE-99145555; PubMed-9990029;
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01-JUL-1993 (Rel. 26, Created)
01-MRR-2002 (Rel. 41, Last sequ
01-MAR-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17374 MW;
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MOD_RES 71 71

BINDING 81 81
                                                                                          FEBS Lett. 221:1-2(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                         S02501; AFMWB.
S02612; S02612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLC25A11 OR SLC20A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxoglutarate
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR;
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RRARRER RRARRE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MALATE OR OTHER DICARBOXYLIC ACIDS, AND PLAYS AN IMPORTANT ROLLE IN SEVERAL METABOLIC PROCESSES, INCLUDING THE MALATE-ASPARTATE SHUTTLE, THE OXOGLUTARATE-LISOCITERATE SHUTTLE, IN GLUCONEOGENESIS FROM LACTATE, AND IN NITROGEN METABOLISM.

SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LQPDPAARYRNVLEALWRIIRTEGLWRPWRGLNVTATGAGPAHALYFACYEKLKKTLSDV 63
INNER MITOCHONDRIAL MEMBRANE IN AN ELECTRONEUTRAL EXCHANGE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00153; mito_carr; 3.
Prosite; PS00215; MITOCH_CARRIER; 2.
Mitochondrion; Inner_membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.4%; Score 79.5; DB 1; Length 313; 31.1%; Pred. No. 0.39; tive 12; Mismatches 49; Indels 1
                                                                                                                                                                        -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> M (IN REF. 1).
A4831A2E1A9F175A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 IHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33930 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X66114; CAA46905.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF070548; AAC28637.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.4%
Best Local Similarity 31.1%
Matches 28; Conservative
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100
139
201
239
239
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MIM; 604165; -.
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313 AA;
                                                                                                                                                     inner membrane
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Run on:

OM protein - protein search, using sw model

August 27, 2002, 04:19:24; Search time 130.92 Seconds (without alignments) 173.101 Million cell updates/sec

US-09-870-113-12 695 1 MOSLQPDPAARYRNVLEALW......QFAEESTSVLVGNSVTLFYH 131 Title: Perfect score:

Scoring table: Sequence:

562222 seqs, 172994929 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

562222

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL_19:* Database :

5: sp_invertebrate:*
6: sp_mammal:*
7: sp_inc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_ordant:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archeap:*
17: sp_archeap:* 1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAKIES		Description	Q96a46 homo sapien	Q9nyz2 homo sapien	0920q8 mus musculu	Q969sí homo sapien	Q91zy0 mus musculu	Q23125 caenorhabdi	Q9vay3 drosophila	Q9nhy6 drosophila	Q94638 onchocerca	Q94634 onchocerca	Q91mj6 arabidopsis	082049 ribes nigru	064731 arabidopsis	014281 schizosacch	Q921p8 mus musculu	וונויספוות מוות וביספט
		ID	Q96A46	Q9NYZ2	092008	096981	Q912Y0	Q23125	Q9VAY3	O9NHY6	094638	094634						
		DB	4	4	11	4	11	2	S	S	Ŋ	Ŋ	10	10	10	٣	11	11
		Query Match Length DB	364	347	338	155	182	312	379	380	303	301	781	289	331	303	320	345
	dР	Query Match	72.7	50.5	50.1	40.3	39.7	31.2	25.7	24.3	24.2	23.9	20.6	20.4	20.0	17.1	16.5	16.4
		Score	505	351	348	280	276	216.5	178.5	169	168	166	143.5	141.5	139	119	115	114
		Result No.	-	7	٣	4	ហ	9	7	80	6	10	11	12	13	14	15	16

Q9bsk2 homo sapien Q27244 caenorhabdi Q9arl9 hordeum vul Q9arl9 hordeum vul Q9awf9 homo sapien Q9ax03 oryza sativ Q9uhr1 homo sapien Q9cq1 homo sapien Q922g0 mus musculu Q922g0 mus musculu Q9ca93 arabidopsis Q9432 arabidopsis Q9432 arabidopsis Q9p182 homo sapien	Q94166 homo sapien Q9bzj4 homo sapien Q9dam5 mus musculu Q9dd91 mus musculu Q9dd98 homo sapien Q9c6k8 arabidopsis Q9hc21 homo sapien Q9m28 arabidopsis Q9fri7 arabidopsis Q9fri7 arabidopsis Q9fri7 arabidopsis Q948k8 mus musculu Q18844 caenorhabdi Q9sh98 arabidopsis Q9vq37 drosophila
4 09BSK2 5 027244 10 09ARL9 4 01489 10 09AX03 10 09AX03 14 09UNB 4 09UNB 11 09C2G0 10 09CA3 10 09CA3 10 09CA3 4 09P182 4 09P182	4 Q9UF66 4 Q9BZA4 11 Q9DAM5 11 Q9DAM5 10 Q9CGR8 4 Q9HC21 10 Q9MZ28 10 Q9FRI7 11 Q9DBR8 5 Q9SF9 5 Q9SF9 5 Q9F9 5 Q9F9 5 Q9F9
3324 3224 3224 3224 3224 3224 3224 3224	351 359 336 337 320 320 348 358 358
24444465 24444466 233333 2333333 24444466 244466 244666 2446666666666	133.66 122.99 122.99 122.99 122.99 122.99
101.5 99.5 99.5 99.5 98.5 98.5 98.5 98.5 98	24 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
114 125 126 127 127 128 130 131	0.000000000000000000000000000000000000

ALIGNMENTS

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Li Q., Eckenrode S., Wang C., Ruan Q., Shi J., McIndoe R.A., She J.;
"A novel mouse mitochondrial carrier protein gene is up-regulated from young to adult NOD mice.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF361699; AAL27990.1; -.
SEQUENCE 182 AA; 19838 MW; 18E2C5E801228693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Li Q., Eckenrode S., Ruan Q., Wang C., Shi J., McIndoe R.A., She J., "Molecular cloning of a novel mictochondria solute carrier protein (MSCP) gene from mouse and human and its down-regulation in mouse spleen during the maturation of the immune system."; submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MITOCHONDRIA SOLUTE CARRIER PROTEIN (HYPOTHETICAL 16.8 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.3%; Score 280; DB 4; Length 15
65.3%; Pred. No. 9.2e-22;
ive 12; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AY022628; AAK30154.1; -.
EMBL; BC015013; AAH15013.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein.
155 AA; 16832 MW; 8ACB98A483C8E6EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                              155 AA
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
MITOCHONDRIAL CARRIER-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=UTERUS, AND LEIOMYOSARCOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 65.3%
Matches 49; Conservative
                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 NDVFHHQGNSHLANG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SDVIHPGGNSHIANG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                 PROTEIN).
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                                                            096981
                      RESULT
Q969S1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li Q.-z., Ruan Q.-G., Eckenrode S., Shi J.-D., Cruz P., Wang C.-Y., She J.-X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A new gene which is highly expressed in NOD mice spleen."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF288621; AAL23859.1; SEQUENCE 338 AA; 37510 MW; BB35B1F70C56A3FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.5%; Score 351; DB 4; Length 347; 67.7%; Pred. No. 8.2e-29; ive 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Indels
                                                                                                                                                                                                                                                                                                               Song H., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
"A novel gene expressed in human hypothalamus.";
submitted (JAN-2000) to the EMBL/GenBank/PDBJ databases.
EMBL; AF223466; AAR64141.1;
InterPro; IPR001993; Mitoch_carrier.
Pfam, PF00153; Mitoch_carrier.
PROSITE; PR001215; MITOCH_CARRIER; UNKNOWN.2.
SEQUENCE 347 AA; 37828 MM; 700DE61B230E001E CRC64;
                                                                                                Last sequence update)
Last annotation update)
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Last annotation update)
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68.8%; Pred. No. 1.6e-28;
11ve 10; Mismatches 19;
                                         347 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0920G8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last and
01-DEC-2001 (TrEMBLrel. 19, Last and
                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Conservative
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-HYPOTHALAMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local Similarity
Matches 64; Conserv
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                                                                                                                                     HT015 PROTEIN.
HT015.
                                       09NYZ2
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                13 MOSLNPDPKARYTSIYGALKRIMHTEGFWRPLRGLNVMMMGAGPAHAMYFACYENWKRTL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophia melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                       31.2%; Score 216.5; DB 5; Length 312; 50.0%; Pred, No. 1e-14;
                                                                                                                                                                                                                                                                                           'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 1e-14;
16; Mismatches 28; Indels
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Swinburne J., Ainscough R.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                    Prem; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 312 AA; 34093 MW; D65FC4DD2936F76A CRC64;
                                                                                                                                       Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                    EMBL; 266521; CAA91399.1; -.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                               Created)
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                                                                                                            PRT;
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG4963 PROTEIN (GH09840P).
                                                                                                                                                                                                                                                                                                                                                                                                         47; Conservative
                                                      PRELIMINARY;
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                                                                                                                                                                          Caenorhabditis elegans.
                                           61 SDVIHPGGNSHIANG
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                        W02B12.9 PROTEIN.
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NCBI_TaxID-7227;
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                                                                                                           923125
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RA Annandraes F.C., Scherer S.E., Lip. P.W., Hoskins R.A., Galle R.F., Gerger R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.

Ra Brandon R.C., Baxter E.G., Helt G., Champen M., Pfeiffer B.D., Ra Brandon R.C., Baxter E.G., Helt G., Champen M., Pfeiffer B.D., Rad M. H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Baldwin D., Ballew R.M., Basu A., An H.-J., Andraws-Pfannach. Delabakov S., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Botchan M.R., Bouck J., Broxettein P., Brottler P., Canter A., Chandra I., R. Borkova D., Botchan M.R., Bouck J., Broxettein P., Brottler P., Canter A., Canley S., Dahlke C., Davenport L.B., Davies P., Buttis K.C., Busam D.A., Danike C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Bodson K., Doup L.E., Downes M., Dugal Rocha S., Dulkov B.C., Ferriac C., Ferriac S., Fleischmann W., Rosler C., Gabriellan A.E., Gary N.S., Gelbart W.M., Glasser K., Gary N.S., Gelbart W.M., Glasser K., Alush F., Karpen G.H., Ke.Z., Kenligon J.R., Houck J., Harris M.D., Houston K.A., Howland T.J., Well M.-H., Ibeeywan C., Jalaih M., Kalush F., Karpen G.H., Ke.Z., Kenligon J.R., Houck J., Merklico G., Milshina N.Y., Mobarry C., Morris J., Wonshrei A., Month S.M., Wolbarty C., Morris J., Worsherson D., Nelson C., Siden Klamen G.S., Edner K., Panne G.S., Pollard J., Puri V., Reese M.G., Relington M., Pittman G.S., Pollard J., Puri V., Rese M., Shue B.C., Siden Klamen E., Shen H., Wang X., Ranne B.C., Siden Klamen D.R., Welson D.R., Welson D.R., Welson D.R., Welson D.R., Welson D.K., Wangssen D.N., Suppet M., Stupes H., Welson D.K., Randington M., Strong R., Sun S., Tactor C., Turner R., Venter E., Wang S., Tao O., Zhan M., Zhong W., Zhong S., Zho W., Zhong S., Zho W., Zhong S., Zho W., Zhong S., Zho W., Shift H.O., The Genece 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MOSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
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STRAIN=Y, CN BW SP.
STAPAIN=Y, N. BW SP.
STAPAIN=Y, N. BW SP.
STAPAIN=Y, N. BW SP.
STAPAIN=Y, Charles D., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunnoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIBCELLIAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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Inner membrane; Mitochondrion; Transmembrane; Transport.
SEQUENCE 379 AA; 41794 MW; F6A20BABA35F5C2E CRC64;
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A.,
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InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
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EMBL; AY060268; AAL25307.1; -
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PRINTS; PR00926; MITOCARRIER.
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Best Local Similarity
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RESULT Q9NHY6

CG4963

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Cathull J., Miller D.J.,
"cDNns from Onchocerca sp. encoding members of the MRS3/MRS4 class of
mitochondrial solute carriers.";
Biochim. Biophys. Acta 1282:179-181(1996).
EMBL; U45997; AAB19036.1; ...
InterPro: IPR001993; Mitoch_carrier.
Pfam; PF00153; mitocerris. 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 301 AA; 34176 MW; COBA8D819FB8EA79 CRC64;
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                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Gaps
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Onchocercidae; Onchocerca.
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37; Indels
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Last annotation update)
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20; Mismatches
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                                                                                                                                                                                                                                                                                                                                   PRT;
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MITOCHONDRIAL SOLUTE CARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
F10K1.26 PROTEIN.
  34; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6284;
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                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onchocerca volvulus.
Sukaryota, Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
NCBI_TaxID=6282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SDVIHPGGNSHIANGAAGCVATLLHDAAMNPAE-----GNDSST--YHSVGSC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       al protein.
380 AA; 41844 MW; 4C9AA524B97F8C6C CRC64;
                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 4.18 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MITOCHONDRIAL SOLUTE CARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.3%; Score 169; DB 5;
38.1%; Pred. No. 1.3e-09;
tive 17; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 168; DB 5;
Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
                                                                          380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 AA
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
MEDLINE=96326580; Pubmed=8703971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.2%;
36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00153; mito_carr; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Conservative
                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 43; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=CANTON-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO(
Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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094638 094638;

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RESULT 094638

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NSHIANGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSCTCISLQFAEESTSVLV 122
                            SS SNSGAHAVSGVEATVASDAVITPMDVVKQRLQLQSSPYKGVVDCV-----RRVLV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 139; DB 10;
; Pred. No. 1.6e-06;
15; Mismatches 41;
                                                                                                                                                                                                                                     331 AA
                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.0%;
36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                      123 GNSVTLFY 130
                                                                                                                             139 EEGIGAFY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 42;
                                                                                                                                                                                                                                                                                                                                                             AT2G30160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thaliana
                                                                                                                                                                                                                                                       064731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        014281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      014281
                                                                                                                                                                                                                                   064731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   014281
                                                                                                                                                                                                                                                           DDT BACK READ BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                         qq
                                                                                      δλ
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                                                                                                                                                                                                                                                         9:
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                                                                                                                                                                                                                                                                                                                        61 SDVIHPGG--NSHIANGAAGCVATLLHDAAMNP-----AEGNDSSTYHSVGSCT- 107
                                                                                                                                                                                                                                                                                                                                                                                                                       123 S----AGDQNNSVAHAMSGVFATISSDAVFTPMDMVKQRLQMGEG----TYKGVWDCVK 173
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                1 MQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotá; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Saxifragales; Grossularlaceae; Ribes.
                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 289;
                                                                                                                                                                                                             ; Score 143.5; DB 10; Length
; Pred. No. 1.5e-06;
16; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfan; PF00153; mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; 2.
Inner membrane; Mitochondrion; Transmembrane; Transport.
SEOUENCE 289 AA; 30383 MW; 56666AB03DCC507C CRC64;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, Act6971; Act80217.1; -. InterPro; IPR001993; Mitcoh.carrier. InterPro; IPR002067; Mit_carrier.
                                                                           Pfan: PF0013; mito_carr; 4.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SECHENCE 781 AA; 87081 MW; 9FB579B9BD746D1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.4%; Score 141.5; DB 1 31.2%; Pred. No. 7.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Woodhead M.R.;
Phesis (1995), University of Dundee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 RVLREEGIGAFYASYRTTVLMNAPFT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. BEN ALDER; TISSUE-FRUIT;
Woodhead M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 -----CISLQFAEESTSVLVGNSVT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRIAL CARRIER PROTEIN. PRIB7.
                                                                                                                                                                                                             20.6%;
33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 31.2 Matches 40; Conservative
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribes nigrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   082049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     082049
    셤
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SEQUENCE FROM N.A.

SERAILE-V. COLUMBIA;

MEDLINE-20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuser C.M., Venter J.C.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                    Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 MOALRSCP-IKPIGIROAFRSIIKTDGPSALYRGIWAMGLGAGPAHAVYFSFYEVSKKFL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MOSLOPDPAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDVIHPGG--NSHIANGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC004165, AAC16956.1; -.
InterPro; IPR01993; Mitoch_carrier.
Pfam: PF00153; Mitocch_carrier.
mito_carr; 3.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_2.
SEQUENCE 331 AA; 35961 MW; A0DE93084BBC8BC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE MITOCHONDRIAL CARRIER C8C9.12C.
SPAC8C9.12C.
SCHIZOSACCHATOMYCES pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE MITOCHONDRIAL CARRIER PROTEIN.
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3;
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                                                                                                                   C STRAIN-972;
Use Colliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Use Colliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUILAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
-:- SUBCELLUILAR LOCATION: OF THREE HOMOLOGOUS DOMAINS.
-:- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
-:- SIMILARITY: BELONGS TO THE MITOCHONDRIAL.
-:- DOMENTIAL.
-:- DOMENTIAL.
-:- DOMENTALIAL.
-:- DOMENTALIAL.
-:- DOMENTALIAL.
-:- DOMENTALIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 NIVNSVIKISSTEGVYSLWRGISSVIMGAGPSHAIYFSVLEFFKSK----INASPDRPLA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 NGAAGCVATLLHDAAMNPAE-----GNDSSTYHSVGSCTCISLQFAEESTSVLVGNSVT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 NVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 PAARYRNVLEALWRIIRTEGLWRPMRGLNVTATGAGPAHALYFACYEKLKKTLSDVIHPG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO RIKEN CDNA 5730438N18 GENE.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.5%; Score 115; DB 11; Length 320; 32.9%; Pred. No. 0.00052; tive 12; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.1%; Score 119; DB 3; Length 303; Best Local Similarity 27.6%; Pred. No. 0.00018; Matches 34; Conservative 21; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2011) + ...
SEQUENCE 320 AA; 35050 MW; F40B5912706583CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL. 69975CDE18107AB5 CRC64;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                NCBI_TaxID=4896;
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Aj303077 Homo sapi
AX61229 Sequence
AF327403 Homo sapi
Aj303078 Homo sapi
AF267854 Homo sapi
AL353719 Human DNA
AK056782 Homo sapi
BC023172 Mus muscu
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1448 bp mRNA linear PRI 02-MAY-2001
mRNA, complete cds, alternatively spliced, nuclear gene for mitochondrial product.
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AY032628 Homo sapi
AC108878 Mus muscu
AC051642 Homo sapi
AC022597 Homo sapi
AF216674 Homo sapi
266521 Caenorhabdi
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1 (bases 1 to 1448)

1 (bases 1 to 1448)

1 (bases 1 to 1848)

2 (Schweyen, R., Iarsson, C. and Suomalainen, A. Characterization of a novel human putative mitochondrial transporter homologous to the yeast mitochondrial RNA splicing
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Pred. No. 6.6e-186;
; Mismatches 0;
Li,F., Nikali,K., Gregan,J., Leibiger,I.
Larsson,C. and Suomalainen,A.
Direct Submission
Submitted (09-DEC-2000) Human Molecular
Health Institute, Mennerheimintie 166, H
Location/Qualifiers
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                                                    1. .1448
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nikali K., Human Molecular Genetics, National Public Health Institute,
Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1322)
Lal,Pr., Yang,J., Yue,H., Hillman,J.L., Tang,Y.T., Bandman,O.,
Burford,M., Baughn,M.R., Azimzai,Y., Lu,D.A., Au-Young,J. and
Patterson,C.
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Pred. No. 5e-164;
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Patent: WO 0078953-A 76 28-DEC-2000;
Incyte Genomics, Inc. (US)
Location/Qualifiers
1. 1322
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/product="mitochondrial RNA splicing protein 3/4"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1889)
Li,F.Y., Nikali,K., Gregan,J., Leibiger,I., Leibiger,B.,
Schweyen,R., Larsson,C. and Suomalainen,A.
Characterization of a novel human putative mitochondrial
transporter homologous to the yeast mitochondrial RNA splicing
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                                                                 Leibiger, B., Schweyen, R.
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                                                 Lases 1 to 1889)
Li.F., Nikali.K., Gregan,J., Leibiger,I., Leibiger,B., Schweyen
Larsson,C. and Suomalainen,A.
Direct Submission
Submitted (08-DEC-2000) Human Molecular Genetics, National Publ
Health Institute, Mennerheimintie 166, Helsinki 00300, Finland
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

HMRS3/4 gene; mitochondrial RNA splicing protein 3/4

Homo sapiens (human)

1-1889 Nikali K.;

RNA splicing protein 3/4 (HMRS3/4

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Homo sapiens gene), 1889 b

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                                                                                                                                                                                               Submitted (12-DEC-2000) to the EMBL/GenBank/DDBJ databases. Nikali K., Human Molecular Genetics, National Public Health Mannerheimintie 166, Helsinki, FI-00300, FINLAND.
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Best Local Similarity 70.3%;
Matches 1094; Conservative 0
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368 Oy 979 420 Db 1449 428 Oy 1039 480 Db 1509	519 RESULT 6 AF267854 548 LOCUS LOCUS 519 ACCESSION VERSION 608 KEYWORDS 519 ORGANISM	RB	FEATURES 788 SOURCE 519	848 CDS 519 908 519	968 BASE COUNT 558 ORIGIN 1028 Query Mat 618 Rest Locs	88 88 48 48		1268
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1244)

1 (bases 1 to 1244)

Div.X., Yang,Y., Gao,G., Xiao,H., Chen,Z. and Han,Z.

Direct Submission
Submitted (25-MAY-2000) Chinese National Human Genome Center at Shanghai, 331 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, People's Republic of China
Location/Qualifiers
                                GGCATGGCTAGTGCCTTCAGGACGGTATATCAAGTAGGTGGGGTGACCGCCTATTTCCGA 1448
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/tissue_type="normal pituitary"
381. 911
                                                                                                                                                                                                                1244 bp mRNA
HOMO Sapiens NPD016 mRNA, complete cds.
AF267854
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1 (shibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
0no,Y., Hotuta,T., Hiraoka,S., Murkakawa,K., Takiguchi,S.,
Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
Wakanatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Single clone region. Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly." 52162
                                                                                                                                                                                                                                                                                       aatttaccagatccctccacagccatcgcatggtctgtgtatgagttcttcaaatacct 1055
                                                                                                                                                                                                                                                                  576 agtggtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgt 635
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                                                                                                                                                                                                                                                                                                                                               636 acgggcagtgtggcaaatgaaggggccggggccttttaccgcagctacaccaccagct
                                                                                                                                                                                                                                                                                                                                                                                   82930 ACGGCCAGTGTGGCCAAAATGAAGGGCCCGGGGCCTTTTACCGCAGCTACACCACCAGCT
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Homo sapiens placenta cDNA to mRNA, clone_lib:PLACE6 clone:PLACE6003850.
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                                                                                                                                                                                      Score 520; DB 9; I
Pred. No. 1.6e-83;
); Mismatches 0;
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RP11-85A1 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                       AL353719 123160 bp DNA linear PRI 25-SEP-200:
Human DNA sequence from clone RP11-85A1 on chromosome 10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMPORTANT: This sequence is not the entire insert of clone RPI1-85A1 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RPI1-85A1 is at 1 in this sequence. The true left end of clone RPI1-483F11 is at 123061 in this sequence. The true right end of clone RPI1-129J12 is at 51589 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                    992
                                                      811
                                                                                                                                871
                                    caggacggtatatcaagtaggtggggtgaccgcctatttccgaggggtgcaggccagagt
                                                                                            aatttaccagatcccctccacagccatcgcatggtctgtgtatgagttcttcaaatacct
                                                                                                                                                                      872 AATCACTAAAAGGCAAGAAGAGTGGAGGGCTGGCAAGTGA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-85A1"
/clone_lib="RPC1-11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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AL353719 AC007643
AL353719.10 GI:15787725
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PRI 31-OCT-2001

linear

source

FEATURES

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

TITLE JOURNAL

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1. .1072
//doganism="Mus musculus"
/db_xref="taxon:10090"
/cloine="MG:37028 IMAGE:4949779"
/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. S month old virgin mouse."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAGAFYRSYTTO
LTMNVPFQALHFMYYEFLQBHFNPQRRYNPSSHVLCCACAGANADAATTPLDVCKTLL
NTQESLALNSNITGHITGMASAFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAMSVYE
FFYLLITKRQEWRAGK"
308 C 263 g 233 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRRA Plate: 60 Row: h Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X., Hulyk, S.W., Hale, S.M., S., Martin, R.G., Muzny, D.M.,
                                                                                                                                                                                                                                                          Direct Submission
Submitted (04-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus, Similar to putative mitochondrial solute carrier, clone MGC:37028 IMAGE:4949779, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                         Contact: MGC help desk
Email: cgapbs remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgebon.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.
Richards, S., Gibbs, R.A.
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92.2%; Pred. No. 2e-80;
live 0; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAH23172.1"
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                                                                       BC023172.1 GI:18606247
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                                                                                                                                               Mus musculus
                                                                                                                         house mouse.
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                                                                                                                                Submitted (124-077-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics&firi.co.jp, Tel:81-488-52-3951, Fax:81-488-52-3952) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA full insert sequencing: Construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and HRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROD 07-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aatttaccagatcccctccacagccatcgcatggtctgtgtatgagttcttcaaatacct 1055
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           Nagai, K. and Isogai, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE6003850"
/clone_llb="pLACE6"
/clone_llb="PLACE6"
/note="cloning vector: pME18SFL3"
i a 405 c 375 g 423 t
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Pred. No. 5.2e-83;
0; Mismatches 1;
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Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
         Nagahari,K., Masuho,Y., Nagai,K. ar
NEDO human cDNA sequencing project
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0y 640 gcagtgtggcaaatgaagggccggggcctttaccgcagctacaccagctgacc 699 11	SULT 10 096351/C CUS RACUS65351 RACUS65351 RACUS6351.2 GI:17 RACUS6351.2 GI:17 RACUSESTON RACUS HTGS_PHASE1, UNCYWAY TAE. WARTHORS MARMANIA D. M. Adams ALSTOOMANIA BENTCH, J. W. Adams ALSTOOMANIA CARTER'M., CAVAZCA CHON, Z., CHOWGHRY CARTER'M., CAVAZCA CHON, Z., CHOWGHRY COYJE, M.D., DAID DANY-CARTCH, J., DOWN, A.L., DING, Y. DOWN, A.L., DING, Y. DOWN, A.L., DING, Y. DOWN, A.L., DING, Y. HAMILLON, K. HARTH HAMILLON, S., KARLEN, HOLINIS, B., HOMSI JOOGRAP, S., KARLEN, LEWIS, L., LI, J., LONISEGG, H., LOZ. MADESBRATI MATLINEZ, E., JAC. MADESBRATI MATLINEZ, E., JAC. MADESBRATI MATLINEZ, E., LI, LICKER, MADESBRATI MATLINEZ, E., LILL MATLINEZ, E., MADESBRATI MATLINEZ, E., LILL MATLINEZ, E., LILL MATLINEZ, E., MADESBRATI MATLINEZ, E., LILL MATLINEZ, E., LILL MATLINEZ, E., MADESBRATI MATLINEZ, E., LILL MATLINEZ, E., LILL MATLINEZ, E., MADESBRATI MATLINEZ, E., MADESBRATI MATLINEZ, E., MADESBRATI MATLINEZ, E., LILL MATLINEZ, E., LILL MATLINEZ, E., MADESBRATI MATLINEZ, E., MATLINEZ, E., MADESBRATI M

size may differ from sequence length bcm.tmc.edu/docs/Genbank_draft_data.html). g draft' sequence. It currently The true order of the pieces order in this sequence record is the contigs are represented as t sizes of the gaps are unknown. atted with the finished sequence ble and the accession number will yen, N., Nickerson, E., Nwokenkwo, S.,
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er, S., Scott, G., Shen, H., Shooshtari, N.,
Sonaike, T., Sparks, A., Stanley, H.,
sonaike, T., Tamerisa, A., Tamerisa, K.,
r. C., Taylor, P., Tamerisa, A., Tamerisa, K.,
r. Williamson, A., Wleczyk, R., Wooden, S.,
Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., 64 bases at least 040 03 bases at least 030 66 bases at least 020 209880; sum-of-contigs estimation 020 bases; agarose-fp estimation in 020 bases; sum-of-contigs estimation in Genome Sequencing Center, Department ics, Baylor College of Medicine, One 030, USA e version replaced gi:15627972. version 0.990329First call to g of 32851 bp in length and length length in length in length in length of 14731 bp in length of 12090 bp in length of 11650 bp in length of 11650 bp in length of 11650 bp in length of 11011 bp in length of 11011 bp in length of 10862 bp in length of 10862 bp in length of 6947 bp in length of 6947 bp in length of 10436 bp in length of 6448 bp in length of 10436 bp in length of 10436 bp in length of 7348 bp in length of 7348 bp in length of 7348 bp in length c.bcm.tmc.edu/ f Medicine mation mc.edu -24M6 stics

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YEFLOBOVNPRBDYNPOSHIISGGLAGALAAAATTPLDVCKTLLNTOENMALSLANVS
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VSTHWTAGAMAGILEHSIMYPVDSVKTRMQSLNPDPKARYTSIYGALKRIMHTEGFWR
PLRGLNVMMMGAGPAHAMYFACYENMKRTLNDVFSHQGNSHLANGVAGSMATLLHDAV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Submitted (20-701-2000) Pathology, University of Florida, 1600 SW
Archer Road, Rm. D6-15, Gainesville, FL 32610, USA
Location/Qualifiers
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Li,Q.-Z., Ruan,Q.-G., Eckenrode,S., Shi,J.-D., Cruz,P.,
and She,J.-X.
A new gene which is highly expressed in NOD mice spleen
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/note="50E12"
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2 (bases 1 to 1429)
Song, H., Gao, G., Peng, Y., Ren, S., Chen, Z. and Han, Z.
Direct Submission
Submitted (12-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai, 201203, China
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Catarrhini; Hominidae; Homo
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Pred. No. 2.3e-68;
0; Mismatches 336;
                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="hypothalamus"
1. 1429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="HT015 protein"
  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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45. .1088
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atcotggagocactgcgtgatgtaccccatcgactgcgtcaagacccggatgcagagtcta
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Homo sapiens

ORGANISM:

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KEYWORDS SOURCE

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Pred. No. 5.5e-65;
0; Mismatches 32;
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93.2%;
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I bases 1 to 401)
Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J., Kassam,A., Rainhard,C., Randazzo,F., Kennedy,G.C., Pot,D., Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M., Labat,I., Leshkowitiz,D., Kita,D., Garcia,V. and Strache-Crain,B. Human genes and gene expression products
Patent: WO 0102568-A 1912 11-JAN-2001;
CHIRON CORPORATION (US); HYSEQ, INC. (US)
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                                             gaacgttcctttccaagccattcacttcatgacctatgaattcctgcaggagcactttaa
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VSTHWTAGANAGILERSIMPEPDSVKTRMOSINPDFRARYFSTYGALKRIMHTEGFWR
PITCLNVMMGGAPHAMTECYENNKRTLNDVFSHQGNSHLANGILKAFVWSWEALL
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 5869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A novel mouse mitochondrial carrier protein gene is up-regulated from young to adult NOD mice (Unpublished 2 (bases 1 to 5869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-MAR-2001) Department of Pathology, Immunology and Laboratory Sciences, University of Florida, 1600 SW Archer Road, Room D6-15, Gainesville, FL 32610, USA
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/organism="Mus musculus"
/strain="C57BL/6J"
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Best Local Similarity 70.1%;
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antirheumatic; antiproliferative; cardiant; vasotropic; cerebroprotective; neuroprotective, antibacterial; opthalmological; gastrointestinal; nephrotropic; gynaecological; vulherary; thrombolytic; gene therapy; cancer; wound; infectious disease; thrombosis; arthritis; infertility; ss.
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18-AUG-1999;
12-NOV-1999;
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Human transport pr
Human polynucleoti
Human polynucleoti
Human ORFX ORF398
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8966.573 Million cell updates/sec
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                                         Compugen Ltd
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 - nucleic search, using sw model
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AAF27733
AAI60661
AAI58875
AAC74843
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AAC33906
AAS02787
AAH22162
                                                                                                                                       August 27, 2002, 00:34:40
                                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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(HUMA-) HUMAN GENOME SCI INC

Human secreted pro CDNA sequence #574 Human mitochondria

Result Š.

Human secreted pro DNA encoding novel Human prostate can Human ORFX ORF2728

Human ovarian tumo Human immune/haema Slackcurrant fruit

Human ovarian PCR-

pro

Human secreted

Human polynucleoti Drosophila melanog Human cDNA 5'-end

Human CDNA clone r Human ORFX ORF2732

DNA encoding novel

immune/haema cDNA 5'-end Human CDNA clone r Human ORFX ORF2730

Human

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Human

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Sequence 1322 BP; 328 A; 376 C; 351
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10-AUG-1999;
18-AUG-1999;
28-OCT-1999;
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                                                                                                                   encoding uncoupling proteins. The nucleotide sequences may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic
                                                                                                                                                or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
                                                                                                          The present sequence is one of eighteen isolated nucleotide sequences
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                                                 Uncoupling proteins and nucleic acid sequences encoding them, useful
                                                         for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders
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   DR;
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   Soppet
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Pred. No. 2.8e-211;
  CA,
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   Rosen
                                                                                       Claim 1; Page 306-307; 343pp; English.
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  Komatsoulis
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nes 988; Conservative
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The present invention provides the protein and coding sequences for 43 novel human transport proteins (designated TPPTs). These can be used in the diagnosis and treatment of transport, metabolic, neurological, reproductive, cardiovascular and immune disorders, and cell proliferative disorders such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; transport protein; TPPT; transport disorder; metabolic disorder; neurological disorder; cardiovascular disorder; reproductive disorder; immune disorder; cancer; ss.
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atcaagtaggtggggtgaccgcctatttccgagggggtgcagggccagagtaatttaccaga
                                                                                                                                                                                                                                                                                                                    teceetecacagecategeatggtetgtgtatgagttetteaaatacetaatcaetaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human transport protein TPPT-33 coding sequence
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99US-0148177.
99US-0149357.
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AR, Azimzai Y,
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              Gaps
                                      gcagatgtacaactcaccataccaccgggtgacagactgtgtacgggcagtgtggcaaaa
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0
Length 1322;
             Indels
DB 22;
      Pred. No. 6.2e-208; Mismatches 6
Score 972.4;
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88.8%;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
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Zhang J;
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Yang Y,
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Mismatches 0
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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                                                                                                                          polynucleotide SEQ ID NO 4650.
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25-APR-2000; 2000US-0552317.
9-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653191.
19-OCT-2000; 2000US-0653191.
29-NOV-2000; 2000US-0593346.
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AAI60661/c
ID AAI60661 standard; cDNA;
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P-PSDB; AAM41505.
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, limmunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as alconised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
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                peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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cytostatic;
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tu C, Xue AJ,
Drmanac RT;
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0552317.
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25-APR-2000; 2
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22-OCT-2001 .

AAI58875;

AAIS8875 ID AAIS XX AC AAIS XX DT 22-0

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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatoriopic; vulnerary; sequences have activities such as: cytostatic; heuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermaclogical; immunosuppressive; antidiabetic; hypotensive; and enclosit or preventing or treating the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graftension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, VIral, bacterial or fungal infection, malaria, autoimmune disorders, acthma, allergies, aplastic annemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antilifilammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
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Pred. No. 1.7e-185;
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12-OCT-1999 AAZ15876;

(first entry)

Human gene expression product cDNA sequence SEQ ID NO:3345,

SS Human; gene, gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; XX KW OS

Homo sapiens

W09938972-A2. XX XX

99WO-US01619 28-JAN-1999;

98US-0072910. 98US-0075954. 98US-0080114. 98US-0080515. 990800-sn86 28-JAN-1998; 24-FEB-1998; 31-MAR-1998; 03-APR-1998; 03-APR-1998

CORP HYSEQ INC (CHIR) CHIRON (HYSE-) HYSEQ I

ö Crkvenjakov R, Dickson M, Drmanac R, Drmanac S; Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA; Jones WL, Kassam A, Kennedy GC, Kita D, Labat I; Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard Stache-Crain B, Sudduth-Klinger J, Williams LT;

WPI; 1999-494092/41.

Novel human genes and their expression products which are differentially expressed in different cell types

Claim 1; Page 1602; 2479pp; English.

The present invention describes a library of human polynucleotides comprising the sequences given in AAZ1253 to AAZ17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ1232 to AAZ1779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides and be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an arrays for diagnostics (which may be used to determine function of an arrays for diagnostics (which may be used to determine function of an arrays for diagnostics (which may be used to determine function of an arrays for diagnostics (which may be used to determine function of an arrays for diagnostics (which may be used to determine function of an arrays for a function of an arrays for determine function of an arrays for determine function of an arrays for determine function of an array array arrays for determine function of an array array array array array array for determine function of an array array array array array array arra encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists.

Sequence 710 BP; 186 A; 187 C; 183 G; 154 T; 0 other;

Gaps ö Length 710; Indels 58.4%; Score 639; DB 20; I 100.0%; Pred. No. 1.6e-133; ive 0; Mismatches 0; al Similarity 100. 639; Conservative Query Match Local Matches

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457 gaaaagttaaaaaaagacattgagtgatgtaatccaccctgggggcaatagccatattgcc qq δ

δy q

989 577 δ

gtggtcaagcagaggatgcagatgtacaactcaccataccaccgggtgacagactgtgta

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Human secreted protein; autoimmune disorder; hyperproliferative disorder; cardiovascular disorder; angiogenesis; nervous system disorder; bacterial infection; viral infection; ss; fungal infection; coular disorder; wound healing; tissue regeneration; epithelial cell proliferation; skin ageing; chemotaxis; 1gG Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Forty one nucleic acid molecules encoding human secreted proteins, usef in the prevention, treatment and diagnosis of cancer, immune disorders,
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Sequences AASO3873-AASO3922 represent isolated nucleic acid molecules and FCR primers of the invention. acid of the invention. Secreted proteins and their related nucleic acids can be used in the diagnosis of or susceptibility to a pathological condition by determining the presence or absence of a mutation in a nucleic acid or the presence or amount of expression of a secreted protein. The sequences are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, coats, horses, cats, dogs, chickens or sheep. The antibodies to the polypeptides can also be used in alleviating symptoms associated with disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). The disorders include autoimmune conclusions of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, anglogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The peptides can also be used to aid wound healing and epithelial cell proliferation, to help prevent skin ageing due to sunburn, to maintain organs before transplantation, to regenerate tissues, in chemotaxis and
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                                                                                                                                                                                                                                                                                                                                                                           a food additive or preservative to alter storage capabilities
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100.0%; Pred. No. 2.5e-119
iive 0; Mismatches 0;
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Matches 57
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                                                                                           Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; gene therapy; antimicrobial; hepatotropic; immunosuppressive; antirheumatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotides encoding secreted proteins useful for treating e.g.
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Pred. No. 7e-115;
0; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                         SH,
                                                               cDNA sequence #574 encoding novel human secreted protein.
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99.0%;
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Best Local Similarity 99.0
Matches 570; Conservative
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                                                                                                                                                                                                                  WO200177291-A2
                                                                                                                                                                                    Homo sapiens.
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Gulukota K,
                               14-FEB-2002
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AAS62787;
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"mitochondrial solute carrier (hMSC-homologue)"
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                                                                                                                                                                                                            Human mitochondrial solute carrier (hMSC-homologue) encoding cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 379..909
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2000US-0241785
28 JUN - 2000; 20 JUN - 2000; 20 JUN - 2000; 20 JUL - 2000; 20 JUL
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cytostatic; gene therapy; vaccine; metastasis; ds.
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100.0%; Pred. No. 6.7e-107;
ive 0; Mismatches 0;
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2000US-0205515.
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                                                                                                       Best Local Similarity 100.
Matches 520; Conservative
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02-MAR-2000;
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AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
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          2000US-0241787
2000US-0241808
2000US-0241808
2000US-0246417
2000US-0246474
2000US-0246476
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         20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
01-0NO-2000;
08-NOV-2000;
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expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haemacopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK854942 to AAK874950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20964 gaccatgaacgttcctttccaagccattcacttcatgacctatgaattcctgcaggagca 21023
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cytostatic; gene therapy; vaccine; metastasis; ds.
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Matches 519; Conservative
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PR 29-SEP-2000; 2000US-0236369. PR 29-SEP-2000; 2000US-0236369. PR 02-CCT-2000; 2000US-0236370. PR 02-CCT-2000; 2000US-0237039. PR 02-CCT-2000; 2000US-0237039. PR 02-CCT-2000; 2000US-0237039. PR 02-CCT-2000; 2000US-0237039. PR 02-CCT-2000; 2000US-0237040. PR 13-CCT-2000; 2000US-0237040. PR 20-CCT-2000; 2000US-0237040. PR 20-CCT-2000; 2000US-0237040. PR 20-CCT-2000; 2000US-0241785. PR 20-CCT-2000; 2000US-0241826. PR 20-CCT-2000; 2000US-024673. PR 20-CCT-2000; 2000US-024652. PR 20-CCT-2000; 2000US-02492. PR 20	PI Rosen CA, Barash SC, Ruben SM; XX DR WPI; 2001-483426/52.
PB 09-AUG-2001. XX XX YX 17-JAN-2001; 2001W0-US01354. PR 31-JAN-2000; 2000US-0119065. PR 24-FEB-2000; 2000US-01184664. PR 04-FEB-2000; 2000US-01184664. PR 12-WAR-2000; 2000US-01184664. PR 16-WAR-2000; 2000US-01184664. PR 17-WAR-2000; 2000US-01184664. PR 17-WAR-2000; 2000US-0118123. PR 07-UN-2000; 2000US-0118123. PR 07-UN-2000; 2000US-0118123. PR 07-UN-2000; 2000US-011816. PR 11-JUL-2000; 2000US-011816. PR 11-JUL-2000; 2000US-011816. PR 11-JUL-2000; 2000US-0118123. PR 14-JUL-2000; 2000US-0118129. PR 11-JUL-2000; 2000US-0118129. PR 22-JUL-2000; 2000US-0118129. PR 21-JUL-2000; 2000US-011819. PR 21-SEP-2000; 2000US-011819.	27-SEP-2000; 2000US- 29-SEP-2000; 2000US- 29-SEP-2000; 2000US-

solute carrier protein; hMSC-o; hypothalamus;

preparation; detection; ss

Homo sapiens CN1269409-A.

mitochondrial

Human mitochondrial solute carrier protein hMSC-o cDNA

(first

04-MAY-2001

AAF59920:

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concers and cancer memorate immunication to the prevention (1) and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) to polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent. (I) proteins and polynucleotides may be used to prevent. (I) and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                           Disclosure; SEQ ID NO 28132; 3071pp + Sequence Listing; English.
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Pred. No. 6.3e-104;
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The invention relates to a novel human mitochondrial solute carrier protein, hMSC-o (AAB60658), and cDNA encoding it (AAF59920). hMSC-o is expressed in normal human hypothalamus tissue. The invention also relates to the preparation of hMSC-o proteins and nucleic acids, and the detection of hMSC-o proteins and nucleic acids.

Sequence 1305 BP; 292 A; 388 C; 363 G; 262 T; 0 other;

sequence represents cDNA encoding hMSC-o.

New human mitochondrion solute carrier protein and its nucleic acid

Claim 1; Page 19-20; 21pp; Chinese

HUMAN GENE GROUP.

(SREN-) SOUTHERN RES CENT NAT

Xiao

Gao X,

Zhang X,

WPI; 2001-050544/07.

P-PSDB; AAB60658

2000CN-0114958

17-MAR-2000;

17-MAR-2000; 2000CN-0114958

11-OCT-2000

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ggactacgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgccgt 242
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                                                                                                                                             tataagaacggagggcctatggaggcccatgagggggctgaacgtcacagcaacaggcgc
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Length 1305;
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Score 434.2; DB 22; Length
Pred. No. 1e-87;
0; Mismatches 268; Indels
 39.78;
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                al Similarity
619; Conserv
 Query Match
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02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive
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                                         cggggccttttaccgcagctacaccagccagctgaccatgaacgttcctttccaagccat
                                                                                             tcacttcatgacctatgaattcctgcaggagcactttaacccccagagacggtacaaccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse ischaemic condition related cDNA sequence SEQ ID NO:1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                         Page 2555-2556; 2690pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-034733/04.
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ABI99871 RESULT

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Claim 2;

genes

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ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                      Length 483;
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                                                                                                                                                                                                            Sequence 483 BP; 127 A; 139 C; 121 G; 96 T; 0 other;
                                                                                                                                                                                                                                                                      24;
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                                                                                                                                                                                                                                                                      Score 417.8; DB 2
Pred. No. 3.9e-84;
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                                                                                                                                                                                                                                                                                                              0; Mismatches
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93.2%;
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                                                                                                                                                                                                                                                                      Query Match 38.2
Best Local Similarity 93.2
Matches 437; Conservative
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(first entry)

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Human ORFX ORF2744 polynucleotide sequence SEQ ID NO:5487.
                               08-FEB-2001
AAC77189;
 The present sequence is one of 3351 sequences in a library of human polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotides and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and preventive interventions. The polynucleotides, polypeptides and produces against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
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                                                                Kassam A;
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mson G, Drmanac R;
                                                                                                                                                                       Library of polynucleotides for diagnosing a cancerous state of a mammalian cell and detecting cancer, particularly of the colon or prostate, comprises 3351 human polynucleotide sequences -
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                                                                                          Leshkowitiz D;
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                                                                               Lamson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                              Garcia PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                          Kennedy GC, Pot D, L
Dickson M, Labat I,
LW, Strache-Crain B;
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Dickson M,
                                                              Innis MA,
                                                                                                                                                                                                                                       Claim 9; Page 818; 1046pp; English.
                                                             Escobedo J,
                                                                            Randazzo F,
, Drmanac S,
                                                                                                              Jones
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Matches 392; Conservative
                                                                                                                                          WPI; 2001-091805/10.
                (CHIR ) CHIRON CORP
                                                                                                           Kita Ď, Garcia V,
                            HYSE-) HYSEO INC
                                                                                            Crkenjakov R,
                                                           Williams LT,
Reinhard C, 1
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; in antiviral; antifungal; antirheumatic; antidiabetic; hypotensive; and nation to, or preventing or treating pathological conditions and nucleic acids may be used to treat cancers; proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malarla, autoimmune disorders, asthma, allergies, aplastic anneamia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiliflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                Vulnerary; antipsoriatic; antiparkinsonian; notropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coaqulation; thrombosis; contraceptive; ss.
Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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Score 380.8; DB 21; Length 1716;

34.8%;

Query Match

AAC77189 standard; cDNA; 1716

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Pred. No. 9.4e-76;
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68.88;
Best Local Similarity 68.8
Matches 539; Conservative
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Search completed: August 27, 2002, 02:35:07 Job time: 7227 sec

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex Michael Brennan
                   US-08-483-533-39
US-09-283-471A-39
US-08-658-136-1
US-08-483-533-36
US-09-283-471A-36
PCT-US31-06532-1
US-08-458-745-1
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US-07-945-283-1
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US-09-773-816-1
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US-09-773-816-1
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US-09-28-1-14-15
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US-09-28-818-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILLING DATE: No. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/09068140A Patent No. 6281409 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Dinner, Dara L. REGISTRATION NUMBER: 33,680 REFERENCE/DOCKET NUMBER: C7C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
TELEFAX: 610-270-5090
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SEQUENCE CHARACTERISTICS:
LENGTH: 5150 base pairs
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Sequence 14,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
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                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-165-264-13
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US-08-403-852D-3
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US-08-893-333-1
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Maximum DB seq length: 2000000000
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                                     Gaps
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                                                                     cgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgccgtggcagg
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                                   27;
 Length 5150;
Score 92; DB 4; Length 515
Pred. No. 3.4e-13;
0; Mismatches 330; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MATY Rose Woodhead, Mark Andrew Taylor
APPLICANT: and Rex Michael Brennan
TITLE OF INVENTION: Blackcurrant Promoters and Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 834 cacaaccccactggacgtttgcaaaacactgctcaacacccagg 877
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 8.4%;
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ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                   Conservative
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                 Similarity
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US-09-068-140A-9
                                   Matches 347;
 Query Match
                     Local
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189 cgaggcgctgccggctggagccactgtcaccacgcacatggtggcaggcgccgtggcagg 248
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YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: NO. 6281409ember 4, 1996
ATTORNEY AGENT INFORMATION:
                                                                             APPLICATION NUMBER: US/09/068,140A FILING DATE:
                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: C70237
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
                                                                                                                                                                                                                                                                                                           33,680
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TYPE: nucleic acid
STRANDEDNESS: unknown
                            SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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Matches 346; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                              NAME: Dinner, Dara L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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MOLECULE TYPE: CD
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APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US,09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
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50.5%; Pred. No. 2.1e-05;
ive 0; Mismatches 138; Indels
 58; Indels
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                                                                                                                                                                                                                                                                                                                                         GENCEAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION:
FILE REPERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 320
 Mismatches
                                                                                                                                                                                123 cggcggcggggaggccggggcctgcaggccc 153
                                                                                                                                                                                                   US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/09165264 Patent No. 6197510
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 93; Conservative
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US-09-165-264-14
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                                                                                                                       834 cacaaccccactggacgtttgcaaaacactgctcaacacccagg 877
                                                                                                                                            Sequence 12, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
APPLICANT: VINDAGRAMOORTHY, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
; CURRENT APPLICATION NUMBER: US/09/165,264
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62.4; DB 4;
Pred. No. 2.1e-06;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                       APPLICANT: Vinayagamoorthy, Thuraiayah TTILE OF INVENTION: Milti-Loci Genomic Analysis FILE REFERENCE: 44747 CURRENT REFERENCE: 44747 CURRENT APPLICATION NUMBER: US/09/165,264 CURRENT FILING DATE: 1998-10-01 NUMBER OF EDG ID NOS: 14 SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                               US-09-165-264-8; Sequence 8, Application US/09165264; Patent No. 6197510; GENERAL INFORMATION:
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Best Local Similarity 63.23
Matches 96; Conservative
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Best Local Similarity
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LENGTH: 318
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                             Length 152331;
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                                                                                                                                                                                                                                                                                            93; Indels
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Best Local Similarity 61.7%; Pred. No. 2.6e-05;
Matches 92; Conservative 0; Mismatches 57;
                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                             Score 58.2; DB 3;
Pred. No. 0.00011;
0; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REPERBNCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 70
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6197510
                                                                                                                                                                                LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                             Query Match 5.3%;
Best Local Similarity 55.1%;
Matches 114; Conservative
                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                               NAME/KEY: misc_feature
                                                                                   SEQ ID NO 16
LENGTH: 152331
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US-09-165-264-7
                                                                                                                  TYPE: DNA
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63 gagccccgggggagtcggcgctgctggacgggtggctgcagcgggggcgtggggccggggggc 122
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COTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-13
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1 Similarity 61.9%; Pred. No. 3.3e-05;
91; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 57.6; DB 4;
Pred. No. 2.9e-05;
0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vinayagamoorthy, Thuraiayah TITLE OF INVENTION: Multi-Loci Genomic Analysis FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
                                                                                   moorthy, Thuraiayah
Multi-Loci Genomic Analysis
                                                                                APPLICANT: Vinayagamoorthy, Thuraiayah; TITLE OF INVENTION: Multi-Loci Genomic Anal; FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 11, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
US-09-165-264-13
; Sequence 13, Application US/09165264
; Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.3%;
Best Local Similarity 58.9%;
Matches 99; Conservative (
                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 91; Conserv
                                                                      ; GENERAL INFORMATION:
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US-09-165-264-11
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APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Blosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
       727 CGGCCAGGACCGGGTCGTCGGAGCCGGTGAGCGCCACCGTGAAGCCGTCCGCGGGGCTGT 668
                                                                                                                                                                                                                                                  119 gggccggcggcggggaggccggggcctgcaggcccccggtacgacaagatccggactccg 178
                                                                                                                                                                                                                                                                                                                    667 ceccescarrcescescescescescescescescescescescererrescerescescerescer 608
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STREET: 1300 I Street, N.W., Suite 700
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 25,146
RECENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY AGENT INFORMATION:
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FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08510646B Patent No. 6077699
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Blanche, Francis
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LENGTH: 833 base pairs
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Lacroix,
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APPLICANT: Blanc,
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US-08-510-646B-3/C
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STATE: D.C
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APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
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STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
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COMPOURE: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PROR APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATONNEY/AGENT INFORMATION:
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REGIGSTRATION NUMBER: 25,146
REEFERNCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 833 base pairs
123 cggcggcgggaggccggggcctgcag 149
                                                                         278 ggggggggggggggggggggggg 304
                                                                                                                                                                                                          US-08-403-852D-3/c
; Sequence 3, Application US/08403852D
; Patent No. 5891695
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Lacroix, Patricia
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Blanche, Francis
Crouzet, Joel
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thibaut, Denis
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan,
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APPLICANT: Blanc,
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ORIGINAL SOURCE
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US-08-403-852D-3
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Sednences
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APPLICANT: Debussche, Laurent
APPLICANT: Debussche, Laurent
APPLICANT: De Creey-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis of Streptogramins, Nucleotide E
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50.6; DB 4;
Pred. No. 0.0018;
                                                                                                                                                                                              03806.0054-00000
            FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORIEX AGENT INFORMATION:
                                                                                         APPLICALL:
ATTORNEY/AGENT INFORMATION.
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.
TELEPHONE: (202) 408-4000
TELEFACOMMUNICATION INFORMATION:
TELEFACOMMUNICATION INFORMATION:
TELEFACOMUNICATION INFORMATION:
TELEFACOMUNICATION INFORMATION:
TELEFACOMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 base pairs
"YPE: nucleic acid
"YPE: "NESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08403852D Patent No. 5891695 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: S.pristinaespiralis
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Thibaut, Denis
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Blanche, Francis
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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APPLICANT: Blanche,
APPLICANT: Crouzet,
APPLICANT: Jacques,
APPLICANT: Lacroix,
APPLICANT: Thibaut,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE
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US-08-403-852D-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-231-818-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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APPLICANT: Blanche, Francis
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Jacques, Nathalie
APPLICANT: Zagorec, Monique
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: Decry-Lagard, Valerie
APPLICANT: Debussche, Laurent
APPLICANT: Coglorer, Valerie
TITLE OF INVENTION: Coding For These Polypeptides and Their Use
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 gcccggactacgaggcgctgccggctggagccactgtcaccacgcacatgtggcaggcg
                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                       Score 50.6; DB 3; Length 833;
Pred. No. 0.0018;
0; Mismatches 114; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/231,818
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                             ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09231818 Patent No. 6171846 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       4.6%;
ilarity 53.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005-3315
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                        MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 ccgtggcaggg 249
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                                  linear
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STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 133; Conserv
                                                                                                 ANTI-SENSE: NO
                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-231-818-3/c
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De Crecy-Lagard, Valerie
FRNTON: Polypeptides Involved In The
FENTLON: Biosynthesis Of Streptogramins, Nucleotide Sequences
FENTLON: Coding For These Polypeptides And Their Use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 gagcc---ccggggagtcggcgctgctggacgggtggctgcagcggggcgtgggccggg 118
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                                                                                                                                                                                                                      STREET: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.6%; Score 50.6; DB 3; Length 5 Best Local Similarity 53.0%; Pred. No. 0.003; Matches 133; Conservative 0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03806.0054-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FF 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION.

ATTORNEY AGENT INFORMATION.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03806

TELEPHONE: (202) 408-4400

TELEFAX: (202) 408-4400

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:

LENGTH: 5392 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                    STATE: COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: S.pristinaespiralis
                                                                                                                  Zagorec, Monique
Debussche, Laurent
                                                       Nathalie
Patricia
                      Blanche, Francis
                                                                                                                                                                     TITLE OF INVENTION: POLYTITLE OF INVENTION: BLOCATILE OF INVENTION: COMMERS OF SEQUENCE: 45 CORRESPONDENCE ADDRESS:
                                                           Jacques,
Lacroix,
                                                                                               Thibaut,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                          Crouzet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-510-646B-1
                                                                           APPLICANT:
                                                                                                                                                        APPLICANT:
                                      APPLICANT
                                                           APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5392;
                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%; Score .v.v. 53.0%; Pred. No. 0.003; ...ive 0; Mismatches 114; Indels
                                                                                                                                                                                                                          SOFTWARES PATENTING SISTEM: C. DOS/MS.DOS CORREST PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D FILING DATE: 10-MAY-1995 APPLICATION NUMBER: PCT/FR 93/00923 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: FR 92/11441 FILING DATE: 25-SEP-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                            ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-510-646B-1/c

Sequence 1, Application US/08510646B

; Patent No. 6077699

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 5392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 133; Conservative
                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3238 CGAGGGCGGG 3228
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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                                                                           Washington
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                                                                                           STATE: D
COUNTRY:
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APPLICANT: Zagorec, Monique
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crcy-Lagard, Valerie
APPLICANT: De Crcy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Goding For These Polypeptides And Their Use
3298 GCTGCTTCACCGAGGCGGCGTCGCCCTCGTCGAGCAGGACGAGGTCGGCGGCGCGGG 3239
                                          179 geceggactacgaggegetgeeggetggagecactgteaceaegeaeatggtggeaggeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Binnegan, Henderson, Farabow, Garrett & Dunner STREET: Blood Street, N.W., Suite 700
STRTE: D.C.
COUNTRY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
FILING DATE: 25-SEP-1993
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: S.pristinaespiralis US-09-231-818-1
                                                                                                                                                                                                                                          Sequence 1, Application US/09231818 Patent No. 6171846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                           Nathalie
                                                                                                                                                                                                                                                                                                                                                                                Patricia
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                                                                                                                                                                                                                                                                                                                        Blanche, Francis
Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  Lacroix, |
Thibaut, |
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                          Gaps
                                              4;
Score 50.6; DB 4; Length 5392;
Pred. No. 0.003;
0; Mismatches 114; Indels 4
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                           Conservative
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                 Similarity
                           Matches 133;
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/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSDRT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCWVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
8371 Email: fliangelifetech.com URL:
http://fullength.invitrogen.com"
150 thers
                BF14313 601788025
BH483098 536233 MA
BL045863 MR3-FN020
AR015770 Mus muscu
BF515180 UI-H-BWI-
AR31276 ZW78h06.r
AR211366 U080b07.y
AR797100 We26610.x
AR797100 We26610.x
AR59845 AL563845
AJ563845 AL563845
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B0041453 B1004453
B1339456 36426 MA
B1304641 AR063B091
A1743110 wg87d01.x
M53634 md15a04.rl
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1.888
/organism="Homo sapiens"
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BF076673
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AA061624
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AL530804
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                                                                                                                                  Description
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                   13736207 seqs, 6748477542 residues
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/note="Organ: brain; Vector: pCWV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is Oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for [ill-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NH_MGC Library."
                                                                     Email: cgapber: dealingly form: cgapber: dealingly form: cgapber: dealingly form: capber: dealingly form: cbn the form: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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High quality sequence stop: 743.
Lloacion/Qualifiers
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98.1%; Pred. No. 4.8e-117.
ive 0; Mismatches 11.
NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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603077989F1 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5169694 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                       Score 692.2; DB 9;
Pred. No. 6.1e-128;
; Mismatches 8;
                                                                                            8; Mismatches
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                                                       63.28;
97.18;
                                                                                            Matches 748; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1131)
NIH-MGC http://mgc.ncl.nih.gov/.
NIH-MGC http://mgc.ncl.nih.gov/.
Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="retina"
//tasue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dr primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0377 row: c column: 07
High quality sequence stop: 753.
Location/Qualifiers
                                                           999
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                                                                                    ACTITIAACCCCCAGAGGGGTACAACCCAAGCTCCCACGTCCTCTGGAGCTTGCGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4504638"
/clone="lib="NIH MGC 94"
                                                                                                                                                                                                                                                                                    mRNA sequence.
BG295496
BG295496.1 GI:13057189
                                                                                                                                                              UTTTAGGACGGTATATCAA 739
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 681)
Peng, Y., Song, H., Huang, O., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu Homo sapiens cDNA ADB clones
Unpublished (2000)
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BI254253 826 bp mRNA linear EST 17-JUL-2001 602974729F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5114190 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies.
                                                                                                                                                                                                                   Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Joass 1 to 826)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       617 accgggtgacagactgtgtacgggcagtgtggcaaaatgaaggggccggggccttttacc 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 ACAACCCAAGCTCCCACGTCCTCTCTGGAGCTAGCGCAGGAGCTGTAGCTGCCCGAGCCA 661
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can left through the I.M.A.G.E. Consortium/LLNL at:
http://magge.llnl.gov
Plate: LLAMI1277 row. i column: 07
High quality sequence stop: 825.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5114190"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="PHI08"
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Pred. No. 5.2e-107;
0; Mismatches 0;
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                                                                                                                                                  mRNA sequence.
BI254253
BI254253.1 GI:14806485
                        Technologies.
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Best Local Similarity 99.8%;
Matches 598; Conservative
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                                                                                                                                                                                         /tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab host="Solls"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
           Chinese Natíonaí Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
186-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
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                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                    Length 681;
                                                                                                                                                                                                                                                                1 others
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                            Email: harzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
Localion/Qualifiers
1. 681
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="AbbArE05"
/clone="lib="AbB"
                                                                                                                                                                                                                                                                                                                    Score 601.4; DB 9;
Pred. No. 6.9e-110;
0; Mismatches 7;
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91.1%;
 Contact: Zeguang Han
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                                                                                                                                                                                                                                                              149
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Manualia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 645)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAMJOSBB row: p column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             964 accgectatttccgaggggtgcaggccagataatttaccagatccctccacagccatc 1023
                                                                                                              724 cacticatgacctatgaattcctgcaggagcactttaacccccagagacggtacaaccca
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                                                     2 GTAATCCACCCTGGGGGCAATAGCCATATTGCCAATGGTGCGGCCGGGTGTGTGCCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          784 agctcccacgtcctctggagcttgcgcaggagctgtagctgccgcagccacaacccca
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High quality sequence stop: 632.
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/db_xref="taxon:9606"
/clone="InxAGE:4549801"
/clone=lib="NHH_MGG_18"
/tissue_type="large cell carcinoma"
/tissue_type="large cell carcinoma"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

En (bases 1 to 986)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/PASazdar
CONA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCMLSU row: m column: 02

High quality sequence stop: 587.

Location/Qualifiers
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Pred. No. 8.5e-107;
0; Mismatches 15;
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Matches 595;
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SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

ACCESSION VERSION KEYWORDS

BG331197 LOCUS

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FEATURES

BASE COUNT ORIGIN

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Mus musculus Sukaryota, Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 855)
1 (bases 1 to 100; Col., 100; Musconti, 100; M
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                                                                                                                                                                                                                                                                                                M. Fatima
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Pred. No. 3e-98;
0; Mismatches 85; Indels 1.
                                                                                                                                                                                                                                                                                             cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 7
High quality sequence stop: 809.
Location/Qualifiers
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602965377F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5120755 5',
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                                                   /organism-"Mus musculus"
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Enkaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi; Enkaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi; Enkaryota: Metazoa: Chordata; Sciurognathi; Muridae; Mus. CE 1 (bases 1 to 817)

RS NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

AL Unpublished (1999)

AL Unpublished (1999)

Email: Gapbar Stmausberg, Ph.D.

Email: Gapbar Stmausberg, Ph.D.

Email: Gapbar Stmausberg, Ph.D.

Email: Gapbar Stmausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Gapbar Armayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11120 row: 1 column: 09

High quality sequence stop: 777.

ESS.

LOCATION LIFERS SEQUENCE STOP: 777.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_l: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
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                                             701
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                                                                                                                                                                                                                                                                                                                                                                                            702 gaacgttcctttccaagccattcacttcatgacctatgaattcctgcaggagcactttaa
                                                                                                                                                               762 cccccagagacggtacaacccaagctcccacgtcctctggagcttgcgcaggagctgt
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/strain="FVB/N"
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/clone="IMAGE:5043992"
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BI103329
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 576)
1 blass I to 576
1 blass I, to 576
1 blas Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B1057218 576 bp mRNA linear EST 15-JUN-2001 QV3-2N0318-230201-558-a01 GN0338 Homo sapiens CDNA, mRNA sequence. B1057218.1 GI:14464748
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                               Gaps
                                                          ggcccccggtacgacaagatccggactccggcccggactacgaggcgctgccggctggag
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817;
 Length
                             Indels
 1.4e-96;
Score 534.6; I
Pred. No. 1.4e-
0; Mismatches
                            0;
48.8%;
                             Conservative
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Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Entaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
E 1 (bases 1 to 927)

NIH-MGC http://mgc.noi.nih.gov/.
L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CONTACT: Robert Strausped by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llh.gov

Llocation/Qualify sequence stop: 812.
                                                                                                                                                                                            D mRNA linear EST 12-JUN-2001
musculus cDNA clone IMAGE:4975441
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/clone="IMAGE:4975441"
/clone="line="nccape_kid14"
/lab_host="bulos (11 phage-resistant)"
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68 TACCAGATCCCTCCACAGCCATCGCATGGTCTGTATATGAGTTCTTCAAATA-CTCATC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: placenta_normal; Vector: puc18; Site_1: Smal ; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwyg Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2-QV3-GN0338-230201-558-a01&t3=2001-02-23&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 575.

Location/Qualifiers
1. 576
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                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
   Shotgun sequencing of the human transcriptome with ORF expressed
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                     sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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/db_xref="taxon:9606"
/clone_lib="GN0338"
/dev_stage="Adult"
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/clone="UNL-P-FN-7"
/dev_stage="ADULT"
/dev_stage
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Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
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Caetano, A.R., Johnson, R.K. and Pomp, D. Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles
Contact: Pomp, D.
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Lines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                        287
                                                                                                                                                                                                         244
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                            Gaps
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others
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                                                            DB 10;
                                                         Score 507.6; DB 1
Pred. No. 3.1e-91;
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Mammalia; Eutheria; Primates; Catarrhini
u
                                                                                          Mismatches
104
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165
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Tue Aug

FEATURES

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/note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I; Five libraries representing EIO:5/12.5 pancreatic bud, EI5.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were seperately constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA was made by oligo-dT priming and Size-selected by Column fractionation. Libraries were amplified once on Solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
                                                                                             1 (bases 1 to 560)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Mara,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Glbbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Onpublished (2000)
Other_ESTS: ic92e02.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
                                                                        Sciurognathi; Muridae; Murinae; Mus
                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 560)
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/dev.stage="Embryonic day 10.5, E12.5, E16.5, newborn, adult, mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library was constructed by Dr. Douglas Melton DNA sequencing by Washington University Genome Sequencing Center For information obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 430.
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/clone_lib="Melton Normalized Mixed Mouse Pancreas
NI-MMS1"
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Pred. No. 3.4e-90;
0; Mismatches 36
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: dmelton@biohp.harvard.edu
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Best Local Similarity 93.6%;
Matches 524; Conservative
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JOURNAL
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                                                                                                       REFERENCE
                                                                                                                                   AUTHORS
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                                                                                                                                                               /organism="Homo sapiens"
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: skin; Vector: pCMV-SPORT6
/note="Organ: skin; Vector
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http://image.llnl.gov
Plate: LLAM10699 row
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98.8%;
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CLone distribution: MGC Gloomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM9146 row: o column: 17

High quality sequence stop: 593.
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 Score
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 45.9%;
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